

**FIGURE 1**

C.CAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC  
'TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCTGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTAATCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCCTTTGGAGTTGCTTGCTTCCAACGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTTCATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLNEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-42

#### **Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

#### **N-glycosylation site.**

amino acids 134-138

#### **Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

#### **N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCGCCGCGCCGCCCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT  
GTTCCCTCTTTCCGGGGTCTCTACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGAACCTGAAACCTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
GGCAGTAATACGGA CTCTTG TAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

## **FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEI  
RSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCCATTCCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACCTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTAAGTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
CTGATCAATAATGCTGGTGTTCCTCGGCTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA  
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTNLMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 9**

CGGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGGTGCGCCACCACT  
GTAGTCATGTACCCACCGCCGCCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG  
CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCTCGTGCTGGAGGAAATGGA  
AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTTACGGCTAGAGGA  
AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAACCAGCAAATCCACCCGTCTTACCAG  
CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGTACAGAAAGACACAA  
AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCCTGTGGATCCCCGCCCCGGAAGGAG  
ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGGACCCGAG  
CTCCCTTCAAGAAGAGCAGAAGTGCCCAACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA  
AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGAAGAAGTTACACTTTGAAAAGGACG  
TGGACGTCAACCTGTTTGAAGCAGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC  
CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCC  
CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTACAGCTGGAGTTCCGG  
GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCAATACCCACAGTG  
GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG  
TGGGGGAGCTTGCCACGGCCGCTTACGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA  
GGGACGCTGGCTCTGGGCGTCTACACGGCCTGCCCGCCAGCCACATGGAGCTGGCCACAGGA  
GCTCATGGAGACTTGTACAGATGAACCGGAGCTGGAGACGGGGCTGAGTCCCGAGATCG  
TGCACTTCAACCTTTACCCCCAGCCGGGCGTCCGGACGTGGAGGTCAAGCCAGCAGACAGG  
CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA  
CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGTCC  
CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGAC  
AAGATGGAGAGCTTCTTCTGCGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCTCTGCCTATCT  
GGACCCCTGCCATAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
CTGGGTCTGTGGCATTTTCCAAGGGCCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCT  
CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC  
CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC  
TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
CTGGCCGCCCCGAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGGCCCCT  
CCAGTGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

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## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN  
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT  
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY  
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLTLIDALDTMWILGLRKEFEEA  
RKWVSKKLHFEKDVVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK  
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
HLLRHSEPSKLTFTVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG  
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
AYVFNTEAHPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACGATGTTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC  
ATCCTGTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC  
GCCCCCTCGGGAATCACAACCTGGGTACAAGACATTTCGCCACCTGCATGACCCAGCCTGGCGG  
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGGCC  
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCTTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTGCTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
GGACCCCCCCTGCCTTCCTGCTCACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR  
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 29-49 (type II)

### **N-glycosylation site.**

amino acids 154-158

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

### **Tyrosine kinase phosphorylation site.**

amino acids 226-233

### **N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG  
 GAGCATGTCCGCGCCGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCCGCCGCTGG  
 GCCCCGCGCCGCGTCTCTGCCCCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
 CTCGCCCCCGCAGGCCCGGGCCCGCAGCATGGAGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGGC  
 GCGGGCGCGCCGCGGGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
 AGGGCGGCGGGCGCCGCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTT  
 GCCCCCAGATACTCTGCCCAACCGCACGGTCACCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCAATCTGGTTC  
 GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG  
 TCATTACGGTCTTTTGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
 CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCTT  
 GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT  
 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTTGAAAAGAACATGATTCACAAC  
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTACGGCTGGATCTACTGGAAATTG  
 GGGCTGTCATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAATGATGTCACTAGAGTTCTTTAT  
 ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACCTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTATTCAACATATTACCCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTTTCGATTATGGGAGGCGGGATCCAGAGGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
 AAGACTATTTACAGTTAAATTAGAAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTTTGACGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
 ACCAGGAAGAAGTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT  
 CTTACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT  
 ATTGTTACATGTGAAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTGCTCCT  
 GATTTTAAGACAATAAGATGTTTTTCATGGGCCCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT  
 ATCAAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTTAAAAAAGTATTTCA  
 TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
 GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCACATT  
 TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG  
 TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC  
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTP  
SHRQVVFEGLSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGIT  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560



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## **FIGURE 17**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA  
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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## **FIGURE 18**

MSRSSKVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAAACCACCACGACGTATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGCTGTC  
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGCCCCCTCTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGTCT**TAAG**ACTCTCCCAAGAGGCTCC  
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCTTTCTCTGTTTTCTCTTCTTCTGCTCTCCCTCCCTCCACCTTTTCTTTCCTTCC  
 CAATTCCTTGCACTCTAACCAGTTCCTGGATGCATCTTCTTCTTCTTCTTCTTCTGCTGT  
 TTCCTTCTGT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTCAAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTGCTGCGCTTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GT  
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAAAAAACATATATATATATAT  
 ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCCTGGGTCCCTAGG  
 CCCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
 CTGTGGTATGAAAAAG

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## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFVKV

### **Important features:**

#### **Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

#### **N-glycosylation site.**

amino acids 66-69

#### **Glycosaminoglycan attachment site.**

amino acids 18-21

**FIGURE 21**

GAACGTGCCACCATGCCAGCTAATTTTTGTATTTTGTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGT  
 CTTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGAC  
 GCCTGGCCAGCCTATGCATTTTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGGCACTACAGTGA  
 CCAAACAGACTGAATTTCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAG  
 ACCATTATTACTACTATGACTAAGGGTCACAAATGGGGTACGTTGATGGAGAGTGATTTGTAAAGAGACTACA  
 GAGGGAGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTAGCCCAAACCTGGAA  
 GAATGAGAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTACTACTTTGGC  
 CTGAGAAAATAGCATGGGATTTGGAGGAGGCTGGGGGAACACCACTTCTGCCGACCTGGGCAGGAGGCATTGAGG  
 GCTTGAGAAAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATT  
 GGTCTTATCAACAGATATGGGCAAGCAAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTA  
 GATGGGACAGTGGTGGGTGATGCAAAGGAAAGAGGTCAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGG  
 TTTGGTTTCCATCTTGCCGAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGCAGAGGGGA  
 AGGGAATCTTAAAGAAAGTCTGGATGCCACACTCTTCTCCTTCTCCTCTTCCCTCTCCTCAGAGGTCTCACT  
 CGTGGTTCTTCATTTCTGCCCTGCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTTG  
 CTTCTCGGGGCTGTCTGAATCTCCATTGCTTTCTGGGAGGACATAATTACCTGTCTAGCTTCTTATCATCT  
 TACATTTCCCTGTAGCCACTGGGACATATGTGGTGTCTCTTCTAGCTCCTGTCTCCTCCTCATGCCTTTGCTG  
 GGTATGGGCATGTTAGGGGGAAGGTCATTGCTGTGACAGGGGGCACTGACTTTCTAATGGTGTACCCAAGGTGA  
 ATGTTGGAGACACAGTGCAGATGCTGCCAAGTCCCGGCGAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCC  
 AGGTCCTCCCTGCATGGTATGCAGCCCCCTCCCATGTTCTGGCCACTTTGTCTTTCTCCTCCCGTTTGCACAT  
 CCCTTTGGAACGTGTTCTGTGAGTACATGCTGGGGTCTCCCCCTTTCTTCCCTTGCTCAGGTGAATCTCAGCCC  
 CTTCTCCCACCCAAAGGTTACATGGATCCTAACTACTGCCACCCTTCCACCTCCCTGCACCTGTGCTCCCTGG  
 CCTGGTCTTTTACCAGGCTTCTCCACCCTCCCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACC  
 AAGCCTACCGCATGGCCCAGGGCCGAGTGGCTCACCTCATTGAGTGAAGGGCTGGAGCAAGCCGAGTGACTC  
 ACCTGCTGCCCTTGAATCAGCCTTTTCTCCTTATTCAGACCTCAGCAGGGGCGAACAAGAGGCTCGCTTTGCAG  
 CAGGAGTGGCTGAGCAGTTTGCCATCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCC  
 ACTGATGACTCCTATGATGAGGACTTTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCCCTGGGGCC  
 GCACCTCCAGGACCTGTTACCCGGCCACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCG  
 ACTGCTCACAGACCGTGTCCCCAGACACCCTGTGCTCTAGTCTGTGACGCTGGAGGATGGGTTGTTGGGCTCC  
 CCGGCCCGGCTGGGCCCCACTGGAGGCCAGGACTCACTCTACAACCTCGCCCCCTCACAGAGTCTGCTTTTCCC  
 CCGCGGAGGAGGAGCCAGCCCCCTGCAAGGACTGCCAGCCACTCTGCCACCCTAAACGGGCAGCTGGGAACGG  
 CAGCGGCAAGCCTCTGACCTGGCCTCTTCTGGGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACA  
 GTGACCCACATCATGCCTGGCAGTGGCATGCATCCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCCAAGTG  
 TGGGCTCAAGGCTCCAGCAGAGCTCCACAGCCTAGAGGGCTCCTGGGAGCGCTCGCTTCTCCGTGTGTGTTT  
 TGATGAAAGTGTGGAGAGGAGGAGGGGCTGGGCTGGGGGCGCATGTCTGCCCCCACTCCCGGGGCTTGC  
 CGGGGGTTGCCCGGGGCTCTGGGGCATGGCTACAGCTGTGGCAGACAGTGTGTTTCTTAAATGCCA  
 CACACACATTTCTCCTCGGATAATGTGAACCACTAAGGGGGTTGTGACTGGGCTGTGTAGGGTGGGGTGGGA  
 GGGGGCCAGCAACCCCCCACTTCCCCATGCCTCTCTCTTCTGCTTTTCTTCTCACTTCCGAGTCCATGTG  
 CAGTGCTTGATAGAATACCCCCACCTGGAGGGGCTGGCTCCTGCCCTCCCGGAGCCTATGGGTTGAGCCGTCC  
 CTAAGGGCCCTGCCAGCTGGGCTCGTGTGCTGCTTCACTTCACTCTCCATCGTCTCTAAATCTTCTCTTT  
 TTTCTAAAGACAGAAGGTTTTTGGTCTGTTTTTTCAGTCGGATCTTCTCTCTCTGGGAGGCTTTGGAATGAT  
 GAAAGCATGTACCCTCCACCCTTTTCTGGCCCCCTAATGGGGCTGGGCCCTTTCCCAACCCCTCCTAGGATG  
 TCGGGGAGTGTGCTGGCGCCTCACAGCCAGCCGGGCTGCCATTACGCAGAGCTCTGTAGCGGGAGGTGGA  
 AGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTTCTTCTAGAGAGGGCCACAAGAGGGCCACAGG  
 GGTGGCCGGGAGTTGTGAGCTGATGCCTGCTGAGAGGCAGGAATTGTGCCAGTGAGTGACAGTCATGAGGGAGT  
 GTCTCTTCTTGGGGAGGAAAGAAGGTAGAGCCTTTCTGTCTGAATGAAAGGCCAAGGCTACAGTACAGGGCCCC  
 GCCCCAGCCAGGGTGTAAATGCCACAGTAGTGGAGGCCTCTGGCAGATCCTGCATTCCAAGGTCACTGGACTGT  
 ACGTTTTTATGGTTGTGGGAAGGGTGGGTGGCTTTAGAATTAAGGGCCTTGTAGGCTTTGGCAGGTAAGAGGGC  
 CCAAGGTAAGAACGAGAGCCAACGGGCACAAGCATTTATATATAAGTGGCTCATTAGGTGTTTATTTTGTCT  
 ATTTAAGAAATTTGTTTTATTAAATTAATATAAAAATCTTTGTAAATCTCTAAAA

## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPF SHPKVHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQT VSPDTLCSSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSL YNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170,  
228-232, 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTTCCCT  
GGCACCCCTCCTGCTCAGTGCGACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA  
CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA  
GAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTGACTTAAAGCTAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs,min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA  
MPESEENARDGIPMDDIPPLRTSV

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domain:**

amino acids 235-262

### **N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311



**FIGURE 25**

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
AGCCCGAAGATTCACATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
CTTAGGCCTTTTATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCAGTTTCTCTGATAGTGACCCTGCAG  
CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC  
TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG  
CAAAGTGGCGAGTGGCAGATATCTGCCTCAAAGTATGTGGTTCGAGAAGACCTAGTTGCTG  
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
CATTAAAGTTTATGGGATACTCAAGATATTTACTCATGATTTACTCTATTGCTTATGCTTT  
AAAAAAGGAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT  
TGGCATTGCTTGTTTTTTGAAGTGAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG  
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC  
GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG  
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAAGTTTTTGTGTAAAATATA  
TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCAATTTGTACAAGTTTCTTGAATTTAGA  
AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA  
CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPSFSDSDPAAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG  
RYLPQTYVVREDLVAVEEIRDVSNLGIFIFYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCCTGTACGCC  
 AAGGAACTGGTCCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCTTGACCCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCTGGGG  
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
 GGGACATGGGGTCCCAGTGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG  
 GAAGCCCAGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGCAGCAGTGTCACCCCCAG  
 TGTCTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGGGGCCCCCAAGTGGTCACCTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTAAACA  
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAACCTCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
 TGTCCACAATATTCGTAGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
 AAAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPPEALDSSRQLQADILAATQNLKSP  
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

**FIGURE 29**

[illegible]

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## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA  
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG  
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM  
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS  
GSQSGSSSGSGSNGDNNNGSSSSGGSSSSSGSSSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW  
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL  
GGSGDNYRGQSSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ  
RSSRIP

### **Signal peptide:**

amino acids 1-21

### **N-glycosylation site.**

amino acids 265-269

### **Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### **Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### **N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

### **Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACC  
 GTGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTT  
 CACTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGCGCAGGAGAGTGAGGGGAAGATGTGTTTCTGAACA  
 AGCTGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTTCTTTCTGGAA  
 GAGGGTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGGA  
 CCAGCAGCTGCTCTACACCTGCTGCCCCACATCGGAGAGCTCCGGAAACTGCTCGCTTCGTGGGTGTCAGGCA  
 GTAGTGGACGGAGTGGGGGCTTCATGAGGAAAATACCCCCACCCTACCACCAGCCTGGGAGCCCAGCCTTCC  
 CAGACCAGCCAGGGGCTGCAGGCACAGCTCGCCCCAGGCCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGAC  
 CGTAGAGTTCTGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGG  
 TGCGCCAGGCAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCCAGCTG  
 TTGGAGATCTTGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAG  
 GAAGAGCCCTGGGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAAC  
 TTGCTGTGGGGCTTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAG  
 GTGAAAGCAGCAGTGAGTCGCACACTTCGAGCCCAGGGTCTGAACTGCTGCCCCGGGGGGAGCGGAGGGGGCTG  
 CTCCCGCGCCCTGACGTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTG  
 GAACAGCTCCTAGGCCAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCT  
 GGCAAAGTGCTCTGTGGAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGT  
 ACAGGCTGGAGAGAGGGCAGGCTCGAAGGCTTCTGCACATGCTGCTTTCTTGTGGAAGGAAGACTTTCAGGGG  
 CCGGTTCCGCTGCAGCTGCTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGA  
 CTTGCTGCTATTCTTGCTACGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCCTGCCTGG  
 GCAGCCTCCACCAGGCCAGTGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCC  
 GAGCCCCACCTGCCAGAACCCAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCCA  
 GAGCTAGGGCTGAGAAGTGGCCCTGCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCCTCACGAGGAGGGCC  
 AAGTGCCCAATGCAGACCCTCACTGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTG  
 ACTGCCTGGCATCCCAACACGCGAATCCTAGAGGAAGGAGAGTTGGCCTGATTGGGATTATGGCAGAAAAGTC  
 CAGAGATGCCAGTCTTGAGTAGAAGAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTG  
 GGCTTGTCAACACAGAATTCAAGCCTCATTTGCTATCCCAGCATCTCTTAAACTTTGTAGTCTTGGAATTCAT  
 GACAGAGGCAAATGACTCCTGCTTAACCTTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTA  
 TCACCAGGAGCTGGACTGCCATCTCCTTATAAATGCCCTAACACAGGCCCGGTCTGGTGGCTCATGCCTGTAATC  
 CCAGCACTTTGAGAGGCCTGAGGTGCGCGGACTGCCTGAGGTGAGGAATTCAAGACCAGCCTGGCCAACATGGC  
 AAAACCCCATCTCTACTAAAAATAAAAAAATTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACT  
 CAGGAGGATGAGGCAGGAGACCTGCTTGAACCTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCAC  
 TCCAGTCTGGGTAAACAGAGCGAGACTTTCTAGAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGA  
 AACCTGACTTTCCCCCTGTACCTTCAGCCCCGTGTCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGAC  
 CAAGCACAGGGCATTAGAGCTTTTAAAGAACTGGTTTTCTTTAAAAAAGGGCGGCCG  
 CCTTAAAAAGGGCTTTTATTAATTC  
 TCCCCACACGATGGCTCCTGCAATCTGCCACAGCTCTGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTTCCCTG  
 AGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTGGCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTC  
 TTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGGAGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCC  
 GTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTGGGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGC  
 CGGTGCTCCTTCYTAGGCCAGTCTGGGGAACTAAGCTCGGGCCCTTCTTTGCAAAGACCAGGATGGGGTGG  
 GTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGTGAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCC  
 TGGAGCGCCTCTCTCTGAGCCTCAGTTTCCCTTTCCGTCTAATGAAGAACATGCCGTCTCGGTGTCTCAGGGC  
 TATTAGGACTTGCCCTCAGGAAGTGGCCTTGACGAGCGTCATGTTATTTTCACTAAGTGTCTGCGACGTTGGC  
 CTGGGCACGTGATGAATGGCCCATGTCCCTCTGCTGCGTGGACGTCGCGGTGCGGAGTGCGCAGCCAGAGGCG  
 GGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCGGGAGGGCCTCACAGGAAGTTGGGCTCCCGCACAC  
 CAGGCAGGGCGGGCTCCCGCGCCCGCCGCCACCACCGTCCAGGGGCGGTAGACAAAGTGGAAGTCGCGCT  
 TGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCGGCAGCGCGTCTGCCAGCTGGAAGCAGCGCCCC  
 TCCACCAGCACGAACAGCCGGTGCAGCT

## **FIGURE 32**

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVVDQQLLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVQTQGEEGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282



**FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCTGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTCAGCAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGTGGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG  
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGTGGTT  
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG  
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA  
 TCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCTAG  
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTTCTTCCCATGAGGCCCTTGTTTCAGAGCCCCAGGAATGGACCCCCA  
 ATCACTCCCCACTCTGTGGGATAATGGGGTCTGTCTCCAAGGAGCTGGGAACCTTGGTGTG  
 CCCCCTCAATTTCCAGCACCAGAAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG  
 CACCCTTCTGCCCACACCAGTTTCCAGTGCGGAGTCTGAGACCCTTTCACCTCCCCCTACAA  
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCCTCCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTGC  
 GCAAACCTCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT  
 CTAGCAGGGAGGTTTTCCAACGTGTGGAGGCGCCTTTGGGGCTGCCCCCTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTCTGGGATGGCTGTCTGGGAGCTGT  
 ATCACCTGGGTTCTGTCCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG  
 GGTGTGTTTGTCTCTCTCTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGAAA

## **FIGURE 34**

MSSNKEQRSAVFVILFALITILILYSSNSANEVVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIH  
YYEPKGPDECVTYIQNEHSRKGNNHFRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCT  
 TGAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCT  
 GGGGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATAC  
 CGTCTGAGGGTAGCAGCTCGAACTAGAAGAAGTGGAGTGTGCGCAGGGACGGCAGTATCTCTTGTGTGACCC  
 TGGCGGCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAG  
 GAATGAGGCCTGAGGTCACTGGCTTGCTCCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTC  
 CCTCAGGTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGAGGCACTGTGATCTTGGGCTGCGTGGTGGGA  
 ACCTCCAAGGATGAATGTAACCTGGCGCCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCC  
 TCATCACCCACGGGACCCCTCGTCATCACTGCCCTTAACAACCACTGTGGGACGGTACCAGTGTGTGGCCCGG  
 ATGCTTGGCGGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGT  
 GCAGCACGTGATTGAAGTGGATGAGGGAAACACAGCAGTCACTTGCCTGCCACCTGCCTGAGAGCCACCCCAAAG  
 CCCAGGTCGGGTACAGCGTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTGATCATGCCCTCAGGG  
 AACCTCCAGATTGTGAATGCCAGCCAGGAGGACGAGGCTGTACAAGTGTGCAGCCTACAACCCAGTGACCCA  
 GGAAGTGAAAACCTCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCT  
 ACCCCCCAGAGGCCCCAACCATCATCGTCACCAAAGGCCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAAATC  
 CCACCCCCACGGGTCACTGGGCCAAGGATGGGTCCAGTGTACCCGGCTACAACAAGACGCGTTCCTGTGAG  
 CAACCTCCTCATCGAACCAACCGAGCGAGGAGTCAAGGCACTACCGCTGCATGGCCGACAATGGGGTTGGGC  
 AGCCCCGGGGCAGCGGTCACTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCAACATGGAGCTATCCCG  
 CTGGTCACTCCCTGGGGCCAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTG  
 GCTGAGGAATGCTGTGCCCTCATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCCTCGCGCTCAGCA  
 TGGGGCCTGAGGACGAAGGCGTCTACCACTGTCATGGCCGAGGAGTGGAGCGGCTTGGGAGCGCCCATGCCGTAGTCCAG  
 CTGCGGACCTCCAGGCCAAGCATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGT  
 ATCACCTTCCAACTCGGCAACCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCAACGTGAG  
 TGGGGCCTGCTTCCCCGAAGTGTCCAGGAGAGAAGGGGCGAGGGGCTCCCGCCGAGGCTCCCATCATCTCAGC  
 TCGCCCCGACCTCCAAGACAGACTCATATGAAGTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCC  
 AATCCTCTACTATGTGGTGAAACACCGCAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTC  
 CAGCCAACCCAGCACCGCTGACCTCACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTAC  
 AACTGTGCGGGGAGAGGGCCAGACAGCCATGGTCACTTCCGAACCTGGACGCGCGGCCAAACCCGAGATCATGGC  
 CAGCAAAGAGCAGCAGATCCAGAGAGACGACCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCACGGCC  
 GCCTCTCCCCCAGAAAGCTCCCGACAGGCCACCCTCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGG  
 ATTCCCCGTGGGAATGGTGGGTTCCTCAATCCAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGA  
 CTGGATTCTGGCCACCAGCGCCATCCCCCAGAGGGGCGAGGGCTCCGTGGAGATCACGGGCTAGAGAAAGGCACT  
 CCTACAAGTTTCAGTCCGGCTCTGAACATGCTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTG  
 GTGTGCGGCTACAGCGGTGCGGTGTACGAGAGGCGCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAA  
 TGAGACCACCATCATGCTCAAGTGGATGTACATCCAGCAAGTAACAACAACACCCCAATCGCTTTTATATA  
 TCTATTATCGACCCACAGACAGTGACAATGATAGTACTACCAAGAGGATATGGTGGAAAGGGGACAAGTACTGG  
 CACTCCATCAGCCACCTGCAGCCAGAGACCTCCTACGACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAG  
 CGAGTTCAGCAACGTGATGATCTGTGAGACCAAGCTCGGAAGTCTTCTGGCCAGCCTGGTCTGACTGCCACCC  
 CAACCTCTGGCCCCACACAGCCGCCCCCTTCTGAAACCATAGAGCGGCCGCTGGGCACTGGGGCCATGGTGGCT  
 CGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGCTGGGCTCCATCGTTCTCATCATCGTCACCTTCAT  
 CCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACATAACAACAGACCTGGGTTTTCTCGAAGTGCCCTTC  
 CACCTCCTGCCCCGTATCTATGGTGCCATTGGGAGGACTCCAGGCCACCAGGCCAGTGGACAGCCCTACCTC  
 AGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATGAATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTA  
 CCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTACGAGCAGAGTGACACCAGCAGCCTGCTGAGGC  
 AGACCCATCTTGGAATGGATATGACCCCCAAAGTCACCAGATCACGAGGGGTCCAAGTCTAGCCCCGACGAG  
 GGCTCTTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTGCTGCAGCCCCATCACGACTGCTGCCAACG  
 CCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCCCCGACAGTCTGTCTCTGGAAGCAGTGT  
 GGGACCCCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCTTGTGCCAGTTGAAGAGGTGGACAGTCTGTGAC  
 TCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCAGCACCCCGTAGGGGCTACGTAGGACAGGAACCTGGAAT  
 GCAGCTCTCCCCGGGGCCACTGGTGCCTGTGCTTTTGAACACCACCTCTCACAATTAGGCAGAAGCTGATA  
 TCCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAGACAGAGAAAATTGGTATTTA  
 TTTTCTATTATAGCCATATTTATATATTTATGCACTGTAAATAAATGTATATGTTTTATAATTCTGGAGAGA  
 CATAAGGAGTCTTACCCGTTGAGGTTGGAGAGGGAAAATAAAGAAGCTGCCACCTAACAGGAGTACCCAGGAA  
 AGCACCGCACAGGCTGGCGCGGGACAGACTCTTAACCTGGGGCCTCTGCAGTGGCAGGCGAGGCTGCAGGAGGC  
 CCACAGATAAGCTGGCAAGAGGAAGGATCCCAGGCACATGGTTTATCATCAGAGCATGAGGGAACAGCAAGGCA  
 CGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAAACATTTTCTAAGATGCC  
 ATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAACCTTCCAGAATCAATAATCCGTGGCAACA  
 TATCTCTGTAAAAACAAACACTGTAACTTCTAAATAAATGTTAGTCTTCCCTGTAAAA

**FIGURE 36**

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP  
RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
ANLQDFKLDVQHVIIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQ  
IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTI IIVTKGQSL  
ILECVASGI PPPRV TWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVVGQPGA  
AVILYNVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
RRALRVLSMGPEDEGVYQCMANEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKQGAPAEAPI I LSSPRTSKTDSYELVWRPR  
HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE  
TSVYVTWI PRGNNGGFPIQSFRVEYKCLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV  
RALNMLGESEPSAPS RPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMI PASNNNT  
PIHGFYIYYRPTSDNDSDYKKDMVEGD KYWHS ISHLQPETS YDIKMQCFNEGGESEFSNVM  
ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSI VL  
IIVTFIPFCLWRAW SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
CANGIHMNRGCPSAAVGYPGMKPQQHC PGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
PPCCLGLVPVEEVDS PDSCQVSGGDWCPQH PVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

**FIGURE 37**

CGGGAGGCTGGGTTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
CCAGGCTCCCGCGGCCGACCCCGCGCAACATGCAGCCACGGGCCGCGAGGGTTCCCGCGC  
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
CACCCCCAAAACCCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT  
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTATGACGGGACT  
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT  
TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAAATGGACACCAGGC  
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT  
CCCCATACCTTGTTCCAGGCCTTGTTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
TGCTGGACACAGTCGGTCCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

**FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS  
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDIILQL  
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV  
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFPYGQLSTSCH  
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTQWLC

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATG  
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA  
GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC  
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGATGGGCTGG  
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCCTCCTT  
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA  
ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA  
GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCCCTTCTGCAGTG  
GTTCTTATCACCACTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGA  
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
CACCACAGCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA  
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAAATTG  
TTTTATTTCTCTCA

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## **FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPGH DVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50



**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTTCATAGGGTCTCGGGTCCCCG  
 AACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGGACCCCAAGTGAGGGGCCCCGTGTTGGGGTCTCTC  
 CCTCCCTTTTGCAATTCACCCCTCCGGGCTTTGCGTCTTCTCGGGGACCCCTCGCCGGGAGATGGCCGCGTTG  
 ATGCGGAGCAAGGATTCGTCCTGCTGCCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGG  
 CAGTTCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAAGCCGCAATCGAT  
 CTGCGGGCATGTACCAAGGACTGGCATTCCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCCTGT  
 AGCAGTGATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTG  
 TCGGAGAAAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTA  
 TCCCAGTTACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAC  
 GGTCACTTACTCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGG  
 GCATGAAGGAGACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCA  
 AAATCTGCAAACAGTGTCCATCAGGGGGAGTCTGTACCAAACAACGCAAGAAGGGTTCTCATGGGCTGGAA  
 ATTTTCCAGCGTTGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGC  
 CAGACTCCATGTGTGTGTCAGAAAATTGATCACCATTGAGGAACATCATCAATGTCAGACTGTGAAGTTGTGTAT  
 TTAATGCATTATAGCATGGTGGAAAAATAAGGTTGAGATGCAGAAGAATGGCTAAAAATAAGAAACGTGATAAGAA  
 TATAGATGATCACAAAAAGGGAGAAAAAACAATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGC  
 CAGTGTTCATTATGCAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAAGAGAACA  
 AGCACACAGTGGAAATTACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTC  
 CTTTCAGATTGCTGATTGCTTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATA  
 CTCCTAGAATAACTTGTATACAAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAACATGGAGCATT  
 GTTAATTTACAAACAGAAAAATTACCTTTTGATTGTAACTACTCTCTGCTGTTCAATCAAGAGTCTTGGTAGAT  
 AAGAAAAAATCAGTCAATATTTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGA  
 CAAATAAATAACAAACAAACAGCCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAAC  
 TGATACAAGACAAAAACAGTTCCCTTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCCT  
 GCTCTGAATGCATTATATTTTCCAACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAATT  
 TTCACAGATGGCAAAAAAATTTAAAGATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCT  
 TAAAGATTGGCCATAACCTATATTTTGATAGAATTAGATTGGTAAATACATGTATTACATACACTCTGTGGTA  
 ATAGAGACTTAAGCTGGATCTGTACTGCACTGGAGTAAGCAAGAAAATTGGGAAAACCTTTTTCGTTTTGTTTCAGG  
 TTTTGGCAACACATAGATCATATGTCTGAGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTC  
 TAAATGAATATCTGCATGGGATTTGCTATCATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTC  
 CGTACTATCCTCAAATTTATTTATTTATAGTGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTCACAAA  
 ATGTAATCTTGAAGTAGACAGAGTAGTGAGGTTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCAT  
 CCAATTTTCTTCCCAAACCTCTGCAGCATCTGCTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTG  
 CGGTTAAAAAATATAAGTAGGATAACTTGTAAACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAAT  
 TCTTTGAAACCACTTTACTACTTTTTTTTAACTTAAGTCTAGTTCTAAATACTTTGTCTGGAGCACAAAACAATA  
 AAAGGTTATCTTATAGTCGTGACTTTAACTTTTGTAGACCACAATTCACTTTTAGTTTTCTTTTACTTAAAT  
 CCCATCTGCAGTCTCAAAATTAAGTTCTCCAGTAGAGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCA  
 ACTTCCACATATATTTACTAAGATGATTAAAGACTTACATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAA  
 ACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGTTGCTATAAGCTTGTGAAATGAAATGGAACATTTCA  
 ATCAAAACATTTCTATATAACAATTATTATTTTACAAATTTGGTTTCTGCAATATTTTTCTTATGTCCACCCTT  
 TTAATAAATATTATTTGAAGTAATTTATTTACAGGAATGTTAATGAGATGATTTTCTTATAGAGATATTTCT  
 TACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGACTTTGTAATTTAGGAAAAATGTATAATAAGATAA  
 AATCTATTAAATTTTCTCCTCTAAAACTGAAAAAATGTAATAAAGATAA

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## **FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRC  
GICIPVTESILTPIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA  
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT  
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC  
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT  
CCTGGTTTGGAGTCCTTTCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTG  
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG  
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCCTCTTATGACC  
AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
GGAACCATCATGAATGGACATGGTGGTGGTTCGAAGTCAGCAGACACTAGACAGTAAGTATAG  
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA  
TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTGTTAAAGCAGCCCTTTTGCTTTTTTGT  
TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT  
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGGAGACCACCCTGGGCAACATGGTGAAACTC  
TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
GTCTGAAAAGA

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## **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
GTIMNGHGGGRSQOTLDSKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24

**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTCAACGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCCGGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGACCGCCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCCCAG  
 ACCCCACACTGGCGCGCGGCCACAACGTCAATCAATGTCATCGTQCCCCGAGAGCCGAGCCCCAC  
 TTCTTCCAGCAGTGGGCTACGTGCTGGCCAGCGCTGCTCTTTCATCCTGCTACTGGTTCAC  
 TGTCTCCTGGCCGCCCCGAGGCGCGCGGAGGTACGAATACTCGGACCGAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT  
 GCAAAT**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCTCCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCCACCCTGGCACAACC  
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG  
 AAGACATTCTTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCTAGCCTCA  
 GGGCAGGAGTCCCCTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTTGGAGGA  
 GGACACTCCCCTCAGAACTTGGCAGCCTTGAAGTTGGGGTCTAGCCTCGGCAGGAGTCCCCT  
 CCTCCTGGGGTGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACATAAAGTCCCCATCTGATTTTAAAAA  
 AAAAA

**FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLLDL  
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPPPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDLDKGFRKENCK

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGACATGCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCCGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGTCTTGCCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG  
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
GGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCAGATTCAATTGATTCCACACACCCCCCTCTCC  
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTGCTGACCTAT  
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGACACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGTCTCCCTGGAATGGA  
AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAAGTGGCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT  
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

**FIGURE 48**

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIFFSLGI  
GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472



**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTCACCAAGAGCTGGAGACACCA  
TCTCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC  
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTACCC  
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
AAGGTGCCCCGAGAAGCTGGGCTACGCCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCGAAGA  
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
CGATGAAGAAGTTTGAAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC  
CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
CGCCGAGGCCCTCCGGGCCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGCTGCTGACGGCGAGCGGACCGG  
CGGTGAAGCGCATCACCTTCTCGCCGCCGTGCCCGCCACATGCAGGAGGCGCTGCGGAGG  
CTGCACTACGTGCCGGCCACCAAGGTGTTCTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA  
GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC  
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCAGCGTTCGCC  
GGCTTGAGCCGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACA  
GCCAGGGTGGCTTTGTGGTACAGCCGCCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT  
CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA  
AA

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## **FIGURE 50**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWRREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGGCCGGCCTTCTGCCTGCA  
TGGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGG  
 AAGAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTT  
 CCTGCTGCTGTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCACTTCCGACCCCCGGCGTTGATCT  
 GCATCCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGAC  
 CTGAACAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAG  
 TTGCTGCTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCT  
 GCTTGGGATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTAC  
 CTGGGTTCTGTCTCTTGCATAAAGGTTATAAATCATCACAGACAGTTTGTGCGCATCTTTGCTCAGAATAG  
 GCCAGAGTGGATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGG  
 GACCAGAAGCCATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCA  
 TTGGTGCTGATAGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGA  
 TGATGACCTGAAGCAAAGAGGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCA  
 AAGAGCACTTCAGAAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTCACCGTGGGACCACA  
 GGTGACCCCAAGGAGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGA  
 GCATGCTTATGAGCCCACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTG  
 TACAGGCTGTTGTGTACAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCCGTTGCTGGCTGACGAC  
 ATGAAGACTTTGAAGCCACATTGTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAA  
 TGAGGCCAAGACACCCCTTGAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGG  
 GTATCATCAGGCATGATAGTTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTT  
 CGTGTAATTGTCACTGGAGCTGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCA  
 GGTGTATGAAGCTTATGGTCAAACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAG  
 GTCACGTTGGGGTGCCCTGGCTTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAATACTTTACAGTG  
 AATAATGAAGGAGAGGTCTGCATCAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACA  
 GGAAGCCCTGGACAGTGATGGCTGGCTTCAACAGGAGACATTGGTCGCTGGCTCCCGAATGGAATCTGAAGA  
 TCATCGACCGTAAAAAGAACATTTTCAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATC  
 TACAACAGGAGTCAACCAGTGTTACAAATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGATGGT  
 GGTTCTGACACAGATGTACTTCCCTCATTTGTCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCC  
 AAAACCAAGTTGTAAGGGAAGCCATTTTAGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAAACTTTT  
 GAACAGGTCAAAGCCATTTTCTTCATCCAGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAA  
 AGCAAAGCGAGGAGAGCTTCCAAATACTTTCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGG  
 ATAAGGTACTTAAGTACCTGCCGGCCCACTGTGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATT  
 TGTTTTGCCTTTCTCCTATTTTTTTTTTAACCTGTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACA  
 TATAATGTGTAACTTAGTTCCCAAATAAATCAATCCTGTCTTCCCATCTTCGATGTTGCTAATATTAAGGCT  
 TCAGGGCTACTTTTATCAACATGCCTGTCTTCAAGATCCAGTTTATGTTCTGTGTCCTTCTCATGATTTC  
 ACCTTAATACTATTAGTAACCACAAGTTCAAGGGTCAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTTGTGATA  
 AACATAACTTGCCAACAGTCTCTATGCTTATTTACATCTTCTACTGTTCAAACCTAAGAGATTTTAAATTTCTGA  
 AAACTGCTTACAATTCATGTTTTCTAGCCACTCCACAAACCACTAAAATTTTAGTTTTAGCCTATCACTCATG  
 TCAATCATATCTATGAGACAAATGTCTCCGATGCTCTTCTGCGTAAATTTAAATTGTGTACTGAAGGGAAAAAGTT  
 TGATCATACCAAACATTTCTAACTCTCTAGTTAGATATCTGACTTGGGAGTATTAATAATTGGGTCTATGAC  
 ATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTACAGTAGGAACTGGGGAGTAAATCTGTTCCCTACA  
 GTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACAGGTGGGCCCAGTGAACTTTCCAGTAAATGAAG  
 CAAGCACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCTACAGGCAAGCAAGATGCCACACAACAGGCTT  
 ATTTTCTGTGAAGGAACCACTGATCTCCCCACCCCTGGATTAGAGTTCTGTCTACCTTACCCACAGATAA  
 CACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAACTATTACAGATAAAAAA

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## **FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNQSVMGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCV E HAYEPTPDDVAISYLPLAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFFAVPRLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGIIRHDSFWDKLI FAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSLVGVVVPD TDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFSSIENGLLTPTLKA KRGE LSKYFRTQIDSLYEHIQD

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 61-80

#### **Putative AMP-binding domain signature.**

amino acids 314-325

#### **N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG  
CCCCGGGGCCCCCTAAGCCATTCTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
CCGGTATGGACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
GACAGGGGGCCGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA  
CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGGCC  
CTAGGCCGCGCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGGTCTCTGGACGTAGA  
GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG  
AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGGCCACGTG  
ATGGCAAACGTTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT  
CAACATGGTAGCGCCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
GCTCAGCAGAAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC  
TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
GTTTACAGCCCTGACCCACTCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAG  
GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT  
CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCCACT  
GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT  
CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCT  
ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG  
TTTCCCGATCCTACCACTTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACGAGGGCC  
TACTTCAAGAAGCACAGTTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
GAAGAAAGAAGCTTATGAAGTGGAAGTTTCAAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
ACAGCAAGAACCCTTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
TTTATTTCGAATGGAGAAAGATGATGACTTCAACACCTGGACCCAGCTTGCCAAGTGCCTCCA  
TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTTCGGAAGAAGA  
ACCACTTCCTGGTGGTGGGGTCCCCGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC  
ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
ATGAGACCTCCTCCAGGACCCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCCTGCTCCAACACCCCGTTCTGAGTT  
AAAAGTCTATTTATTTACTTCTTGTGAGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA  
ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTT  
TTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCTTA  
GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTGTCCAGATTTCAAAGCTGGATAAGTT  
GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVNIKLILDTR  
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
REQGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK  
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS  
AEEAECHWADTELNRRRRRFC SKVEGYGVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPM DVVALFGLRGIQHTPISIKNARVSQHY  
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS  
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVD SLKKEAYEVEVHRL LSEAEVLDHS  
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNH  
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACA  
 CCTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAA  
 TAAAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATG  
 TTACGTGGCCGGAATCATTCCCTTGGCTGTAAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTT  
 TTGGGTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCTGAAGGAGTACATGCCCTTT  
 ATGAAGATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAA  
 AGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTAT  
 ATTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATG  
 TGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCT  
 GGTGTCCATGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTC  
 CAGTTAATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCT  
 TGATGCATGCTGGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACC  
 AGTTATGTCCATGGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAGCCCTTTTCCAGAGGTGAAC  
 GCCACGGGAGTGGCCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCC  
 CTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCT  
 GGAAGTGGCAGCCCTGGTTCTGGGTTGCCTCATCCCTCTCATCCTGTGCTAGGACACCAGCATTAA  
 ATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGC  
 TACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGG  
 AGGTGAGGTTAAAACCTGAGTAATGGAAAAGCTTTTAGAGTAGAAAACACATTTACGTTGCAGTTAGC  
 TATGACATCCCATTTGTGTTATCTTTTAAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAA  
 CCTATTCTCAGGGAAGATGGAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAA  
 TAGTGATTATGAAAATACAGTGTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCT  
 GCTACTTTATCCATTGATTTTTAACATGGTTCCCACCATGTAAGACTGGTGTCTTAGCATCTATGCC  
 ACATGCGTTGATGGAAGGTCATAGCACCCTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGG  
 GATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCA  
 TTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGC  
 CATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCAT  
 TCCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGTA  
 GTTTTCAGTTCTAGGCTTTCTTCAAGAACAGTCAGATCACAAGGTGTCTTTGGAAATTAAGGGATAT  
 TAAATTTTAAAGTGATTTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAA  
 AATGTATGGTTGTCTTTTTTTTTTGTTTTTTTTTTTTTTAAATTATTTCTCTTAGCAGATCAGCAATC  
 CCTCTAGGGACCTAAATACTAGGTCAGCTTTGGCGACACTGTGTCTTCTACATAACCACCTGTAGC  
 AAGATGGATCATAAATGAGAAGTGTTTGCCATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTC  
 TCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTTTCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCT  
 TACTGCTGGTGTAAATATTTGTGTGGGATGAATTCTTATCAGGACAACCACTTCTCGAACTGTAATA  
 ATGAAGATAATAATATCTTTATTCTTTATCCCCTTCAAAGAAATTACCTTTGTGTCAAATGCCGCTT  
 TGTTGAGCCCTTAAATAACCACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAATTTAAA  
 CAATTGAGATAGCAAAGTGTTTAAACAGACTAGGATAATTTTTTTTTTTCATATTTGCCAAAATTTTTG  
 TAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCAT  
 TTCAAACACATTACACTAAGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTG  
 TAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATGATTTATTTCTTCATGAATTTGTCACT  
 GGATCAGCAGCTGTGGAAATAAGCTTGTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAA  
 TAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACAATTTTACTACCAAGAGAAGGTATAG  
 TATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCTGACTGGTGTGAGACTTGAGGTTTC  
 ATCTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCTGGAAACTGACTTTGTCAAATAAATAG  
 CAGATTGTAGTGTCAAAAAAA

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## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGI I PLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTGLLVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



**FIGURE 57**

GCTCGAGGCCGCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA  
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
GGAATTACGGCAGGCTGCAGCAGGATGTCTTCCAGTTTTCAGAAGAACCAGACCAACCTGGAG  
AGGAAGTTCTCTTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA  
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
CCAGGCCGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACAGGGCCGAAGAGATGACTA  
TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATC  
TGA

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## **FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTACGCTGGCATTGCCCTCTTC  
 ACCAGTGGCTTCTGCTCACCCGTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGT  
 CCTGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGC  
 TGATAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTA  
 CCCTTCTGGGCAAACCTAAGCTCCTTGACAGAGGATCCTGGAGATTAGCCCCACCATGCCCGGCTCTACCGATC  
 TCAGGTTGACCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCAGTGGCTCACTGCCTACCTTTATTG  
 ATGCTGGTAGTAACCTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGG  
 CGTGTAGTCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCC  
 ATCCTTCAATGTAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTG  
 GTGAATGGGACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCT  
 GAAATGGCCAAGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACT  
 GCTGGTAGTGGCTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAG  
 CTGCTCTCTTTCTGTATAGCCCCACAGCAGTCTTCCCCAGCACCCCCACAGAGGAGCCAGAGGTGATTCTCTCAA  
 GTTAGCCTTGTGCCACGCTGGCCCTGCTGCTGGGCCTGCCCATTCCCATTGTGGGAATATCGGGGAAGTGATGGC  
 TGAGCTATTCTCAGGGGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCA  
 ATGCTCAGCAGGTGTCCCGATTTCTTCATACCTACTCAGTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCAT  
 CAGCTGCAGAACCTCTTCTCCAAGGCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGC  
 GACACTGCCGACTGTGATTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGG  
 CTCGTTTCTCTCTGGTCCGCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCCTGCTGGCA  
 TCTCAGTGGGCAATATCCCCAGGCTTTCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGG  
 GGCCATAGCGTATGTGGACTCCTGGGAACATTAGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTG  
 CAGTGAGCTCATTTCCCTTTTCTGTGGAAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCTG  
 TTTCCCATCCCTGGGCCCCGTCCTGTTACTCCTGCTGTTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTGT  
 AGCTGAGGCCAGGGCCACCCCTTCTTTTGGGCTCATTATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGG  
 GCCAGCTGCTTCCACCTAAGCTACTCACAATGCCCGCCTTGGCATTTCAGCCACAACAAACCCCCACGGCAC  
 AATGGTGATATGCCCTGAGGCTTGAATTTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTG  
 CCCTGAAGAGACACCTGTTTGCCACTCCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGTGGTCCAGCCA  
 AGAATTTATGGTATGGAGCTTGTGTGGCGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGC  
 TATGGTAATCTCAAGAGCCCCGAGCCACCCATGCTCTTGTGCGCTGGGGACTGCCCTAATGGCATTGGGTAC  
 TGCTGCCTACTGGGCATTGGCGTCGGGGGAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGGCAT  
 CCATGGTGCTGCCCTCGGGCTGTAGCAGGGCTGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACA  
 GTGCTGGTGAAGGCTGGGGCAGGCGCTCCAAGGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTC  
 TCAAGCTGACTTGGATTATGTGGTCCCTCAAATCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGA  
 GGACCAAATCTCAGGGTCCCCTGACTGTGGCTGCTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACA  
 GCCCTCACCTGTTGGCCTTCCCACTTCTGCTGTTGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTT  
 TCTGCAGAGCTTCTTCTCCTACATCTGCTTGTGCTGGGATACCCGTCACCACCCCTGGTCTTTTACTGTGC  
 CATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCACACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTT  
 CCAGCCATCCATTGGCATGCAGCCTTCTGGGATTCCCAGAGGGTTCATGGCTCCTGTACTTGGCTGCCTGCTTT  
 GCTAGTGGGAGCCAACACCTTTGCCTCCCACCTCCTCTTTGAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTT  
 TCCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGCCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCC  
 GAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGGATGCGCCTCAGCACTTCTATGCAGCACTGCTGCA  
 GCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTAGATTCTGGCCTGTGCCTTGGCAGCCTCCATCCTTCGCA  
 GGCATCTCATGGTCTGGAAAGTGTTTGGCCCTAAGTTTCATATTTGAGGCTGTGGGCTTCATTGTGAGCAGCGTG  
 GGAATTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTGTGCTGTGAGCTCCTGGTTCAGGCAGCTATTTCT  
 GGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCTACAGAGAGTGCTGGAGAACAGTGATAGCCTG  
 GCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATACTCTTACTATCATGCAGCCAGGGGCCGCTG  
 ACATCTAGGACTTCATTATTCTATAATTACAGGACCACAGTGGAGTATGATCCCTAACTCCTGATTTGGATGCAT  
 CTGAGGGACAAGGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGGGCGTGGTGACTTGCACCTATAATCCCA  
 GCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCAAGACCAGCCTGTGGAACATAACAAGA  
 CCCCCTCTCTACTATTTAAAAAAAAGTGTAATAAAATGATAATAT

**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQKPGACW  
MASRFSRVVLVLIDALRFDAQPQHSHPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVHDHCGHKHGPHHPM  
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST  
PPEEPEVIPQVSLVPTLALLLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ  
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPCPLLLTPVAWGLVGAIA  
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLLFRLA  
VFFSDSFVVAEARATPFLLGSFILLVVLHWEQQLLPKLLTMPRLGTSATTNPPRHNGAY  
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAAYWALASGADEAPPRLRVLVSGASMVL  
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
LLHLLAAGIPVTTGPFTVPWQAVSAWALMATQTFYSTGHQPVFPPIHWHAAFVGFPEGHGS  
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKRQPPGNEADARVRPEEEEEEP  
LMEMLRLDAPQH FYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG  
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT  
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGTATTTATGGAAATGAATTTGACAAAA  
GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAAACCGGAAGGTACTTCT  
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA  
ATATGATGTGAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG  
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC  
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
AAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
TATATGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAC  
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT  
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAG  
TGGGTGT

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## **FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDF  
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYEDVRTTDICAGPEEQELSL  
QEEVSTQGTLLSQAAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCCTGAGTACTGCGGAGCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGACCCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGCGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCCTTGAGCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAAAAAAAAAAAAAAAAGAAA

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## **FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**

amino acids 1-30



**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG  
CAGGCGCCGCGCTGCTGCTCAAGGACTATGTCAACGGTGGGGCTTGCCCCAGCAAGGCCACC  
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT  
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT  
GCCAGAGCAAGCTCGCCATCGTCCCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCCTCTTCTGGCTGCTGGTCAAGA  
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCCGAGGAACTGGCGGATGTT  
TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGCCCCGAGGCTGAGGATGAGGA  
GGTGGCCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
GGGAGCAGCCCCCTCCCCAGATTAACCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG  
GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC  
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG  
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
GGTGTGTTGCTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC  
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCCAACAGCTGCTGCTACAGGACCTGGGA  
TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC  
TTGCTCATTT

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## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN  
AGVMRCPHWTTE DGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGCATGTGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
CAGCGTGGCGCGCGCCCTGGCGCCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT  
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA  
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
ATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
TGAGGCTGTCATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
TATGTCAGACCCTGGGTTCCCAGCCCCTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT  
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA  
GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
TGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC  
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
GGTGGAAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
GCTGGCTGTCCTGTCCTGGTGGGAGATAAGTGGTGGCCAACAAGTGGATACATGAGTATGG  
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACTTGAACTGTTGGCAGAGAGAAGC  
TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTCT  
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
CAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT  
TTTAAGTTGAAAACAACTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
ATGTTTATAAATCAAAA

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## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAAYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT  
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC  
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTATGGTCTCCTTCATTGGT  
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT  
CTGCCTCATCATGGAGCTCATTTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA  
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACCTATCGAC  
AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
ATGCTGCTTGTGCTACCCCAATTAGGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCCCTCTGCCCACA  
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA  
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC  
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA  
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACAGTTTGTAA  
TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

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## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIILILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL  
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
CACCTGGGAAGATGGCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCTCAGTGACTGTGCCACCAGCCA  
TGGGAGCCTGCGCATCCAAGTCTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
AGGTCAATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT  
AGCTCTACCTGGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTTCAAGCTCATCGTGAGTCA  
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTGG  
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTCCTCCA  
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTCATTGGTG  
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM  
REKPAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGD TIQLYL  
GAKLLDSQGKVTKWFNNSAASLTMP TLDNIPFSLIVSQDVVKA AAVLSPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTLGIEASSEAQFYTKGDQLILNLN NISSDRIQLMNSGIGWFQPDVLKNIITEI IHSIL  
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLTPASLWKPPSPVVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
CTCCAACATGCATAGACAGTGTGTGTTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
AACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTTTTG  
ATGAAGGCTCTGATGTATTTTCAAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACTTT  
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGC  
TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGTCTTTATG  
TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
CCATACAGCTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC  
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA  
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
CCCAGTGAACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA  
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC  
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
ACTTTACGCATCTTTCTTTTGGAGTAGAGAAATTATGTGTGTGTCATGTGGTCTTCTGAAAATG  
GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA  
GATTTTCAGATTCAATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA  
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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## **FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWTKRNPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

### FIGURE 75

[illegible]

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS  
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVY  
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
ILPQLFDLSSDPDEL TNVAVKFP EITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416, 498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
GCCTCTCTTGCCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTTGTGACAG  
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCAGGCCATGAT  
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
ATCCTTGAGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC  
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTC  
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCCTG  
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATTGCTGG  
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC  
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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## **FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGLQLVG YILG LLLG LTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILG LLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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## **FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCAGCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG  
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCT**TGA**GAAAGACATAGAAAGAAAATCAACTTTCACCTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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**FIGURE 80**

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25



**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATT  
CTGTGACCTGTCTGAGGCCCCACCCTGCAGCTGCCCTGAGGAGGCCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGAACCCTTCACCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

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## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGACGCGCTCACTCGCTCGCACTCAG  
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCCCGCGCTCCCCGGCACCAGAAGTTCTCT  
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC  
CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGGCAGAACGTCAACCCTCACCTGCAGGCTCT  
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
CCATGGTGGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT  
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
CTCCAACCGCCGTGCCCAGGAGCTGGTGC GGATGGACAGCAACATTCAAGGGATTGAAAACC  
CCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC  
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCTCAACCCCTC  
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGTCTGAG  
ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCCAGGCTGCTCTTCTGTC  
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTAAAGTCAAT  
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC  
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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## **FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK  
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGQHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCC  
TTTCTGCCCCACCGCTGCTTCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA  
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTC  
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCCGCC  
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT  
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCCACCAAAGTCCTGCC  
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC  
CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGGCCCGGGCACCCAGC  
CCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
GCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG  
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
ACCCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA  
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT  
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG  
AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
CAAAGTGACCAAGACATAACAAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

Country	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050
Japan	7	8	10	12	14	16	18	20	22	24	26
Germany	10	11	12	13	14	15	16	17	18	19	20
France	11	12	13	14	15	16	17	18	19	20	21
Italy	12	13	14	15	16	17	18	19	20	21	22
Spain	13	14	15	16	17	18	19	20	21	22	23
Sweden	14	15	16	17	18	19	20	21	22	23	24
Belgium	15	16	17	18	19	20	21	22	23	24	25
United Kingdom	16	17	18	19	20	21	22	23	24	25	26
Canada	17	18	19	20	21	22	23	24	25	26	27
United States	18	19	20	21	22	23	24	25	26	27	28
China	19	20	21	22	23	24	25	26	27	28	29
India	20	21	22	23	24	25	26	27	28	29	30
South Africa	21	22	23	24	25	26	27	28	29	30	31
South Korea	22	23	24	25	26	27	28	29	30	31	32
Poland	23	24	25	26	27	28	29	30	31	32	33
U.S.S.R.	24	25	26	27	28	29	30	31	32	33	34
Uganda	25	26	27	28	29	30	31	32	33	34	35
Kenya	26	27	28	29	30	31	32	33	34	35	36
Malawi	27	28	29	30	31	32	33	34	35	36	37
Zambia	28	29	30	31	32	33	34	35	36	37	38
Sierra Leone	29	30	31	32	33	34	35	36	37	38	39
Guinea	30	31	32	33	34	35	36	37	38	39	40
Senegal	31	32	33	34	35	36	37	38	39	40	41
Ghana	32	33	34	35	36	37	38	39	40	41	42
Nigeria	33	34	35	36	37	38	39	40	41	42	43
Yemen	34	35	36	37	38	39	40	41	42	43	44
Algeria	35	36	37	38	39	40	41	42	43	44	45
Libya	36	37	38	39	40	41	42	43	44	45	46
Chad	37	38	39	40	41	42	43	44	45	46	47
Cameroon	38	39	40	41	42	43	44	45	46	47	48
Cote d'Ivoire	39	40	41	42	43	44	45	46	47	48	49
Benin	40	41	42	43	44	45	46	47	48	49	50
Niger	41	42	43	44	45	46	47	48	49	50	51
Mali	42	43	44	45	46	47	48	49	50	51	52
Guinea-Bissau	43	44	45	46	47	48	49	50	51	52	53
Sierra Leone	44	45	46	47	48	49	50	51	52	53	54
Liberia	45	46	47	48	49	50	51	52	53	54	55
Sierra Leone	46	47	48								

**FIGURE 87**

[illegible]

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## **FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18



**FIGURE 89**

[illegible]

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## **FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDEQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAG  
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT  
CCGTCACCTCTCCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG  
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCT  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTTCAGGGGCCAGTTCTCTAGCGTGG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
TCTGGGAGCTACAGGTGTCTGAGTCTGAGTCTCCTCTCATTTCATCACGGGATATGTT  
GATAGAGACATCCAGCTACTCTGTCTGAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
GAAAGGTCCACAAGGACAGGATTTGTCCACAGATCCAGGACAAACAGAGACATGCATGGCC  
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGACGCCGGGAGCATATCCTGTTCCATG  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAAGTGGAC  
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
ATCATGGGTACTGGGTCTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGAATATGAGTG  
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCCGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCC  
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGCAACAGTGAGTCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
ACATGGGAGTCAGGTGTCTGAGTCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGQDLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRLNGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSSQATTPFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTCGGAGGCTTCCTTGGTTCGGATTGCA  
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
CCGTGCGCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
GACGCGTCGCCGGGCCCCGGGTTCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC  
TCCACGGCCCCAGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG  
CGACTTCTCCAGCCCAGTCCCCGAGACCAACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCAACCCCTCCGGCGGCGGAACGCACCTTC  
GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCAACCCCTTTCGACGACCACTGGCCCCGG  
CGCCGACCAACCCCTGTAGCGACCAACCGTACCGGCGCCACGACTCCCCGGAACCCCGACCCCC  
GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
TTCGCCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC  
ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGCAACAGAGGGTGGAACCTGAAGTTTATT  
TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT  
TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG  
AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT  
AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA  
ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA  
TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTTGAGACCAAAAG  
TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
ATAATGTACTGTTATCTAAGCATTTGCCTTGTAAGTCACTGAAAGTAATTATTCTTTGACCT  
TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT  
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC  
CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTTCTCAAG  
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
TTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAAATGTAGAAG  
AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

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## **FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRLPSLGGLALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTDLPSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**AT**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTCATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

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## **FIGURE 96**

MGGLLLAAFLALVSVPRQA VVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGWVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20



**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC  
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
GGCTGGATTTACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGGCACAGTATCCACAGTCTTGGG  
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
ATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
AGAGCAAAGCCACATCAGGAGTGA CT CAGGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTG  
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG  
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGT CAGGGGTTCAGCCT  
CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
ACAGATTGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA  
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

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## **FIGURE 98**

MLLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNKYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVSPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLLIPQPQDHGTS LTCQVT FPGASVTTNKT VHLNVSYP PQLTMTVFQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGD TGIEDANAVRG SASQG PLTEPWAEDSPPDQPP PASARSSVGE GELQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCCGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTTCCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG  
CAGCCCCCGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

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## **FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:**

**Signal peptide:**

amino acids 1-17

**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA  
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT  
AAGAAACCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW  
AVRPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLR CANITII EHQKCENAYPGNITDTM  
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDW IQETMKNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

#### **N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

#### **Glycosaminoglycan attachment site.**

amino acids 145-148

#### **Kringle domain proteins.**

amino acids 197-209, 47-64

#### **Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

#### **Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTTGGTGTTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTTAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYWLGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNDHHDGDFISPKEYNVYQHDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



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## **FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

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**FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

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**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCAATGG  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGAGTCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACTTCTTGGAACCTT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**  
GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTTCGGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAAGTGAGGCCTG  
GGGTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACC**AT**GGCCCCCGGGTGGGCAGGGGTTCGGCGCCGCCGTGCGCGCC  
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT  
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCAGCCCCCACTCGGAGCCCCCATCTTGCAATGCCAACTCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCCTGCCA  
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCCCTGATGGGAACA  
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCGCTGCAGCAGCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGGAGAAGTGTGCG  
TGTGAGGGCAGGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
GGAGACCGTGACGGGCGCGTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCTGGGGCCTTCACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCCTGAAGG  
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCACTGCTCCTGCCCTC  
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
AACAATGCCACCTGCGTGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC  
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTGAGCATG  
AGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCCACAAGTGCCGCCACGGGGCCCAGTG  
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG  
AACACCCCCCACCCATGGTTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCCG  
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
CCTCCGCCAAGGTCCGACCCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGGCCACGT  
GCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA  
ATGATGGGCAGTTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG  
GACAAAGGAACCTCAAAGAGCCTGGGGAAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG  
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACCAGGCTGCAAGTCCTGCACCGT  
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCCAG  
GCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
GGAATTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG  
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT  
GTGGGCCCCAGTGCTGCCAGCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG  
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTT  
CTAAGGCCCTGCCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAA  
AAAAAA



**FIGURE 112**

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNKLQVL  
PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
TLNNNNNISRLVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNOISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
GLFDGLVSLQLLLLNNANKINCLRVNTFQDLQNLNLLSLYDNKLQOTISKGLFAPLQSIQTLHL  
AQNPFFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR  
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL  
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCD CSLRWL  
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT  
CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIP L  
DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV  
LLQTSPCDQYECQNGAQCIVVQEQPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC  
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD  
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCCTTAAACTGGAAGCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

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**FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDAAICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

**FIGURE 115**

CAGGCCATTGTCATCCCCTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCC  
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT  
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG  
CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
TTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAAATCTCC  
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT  
CCATTGACCACAGTGTACAGGGTTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA  
ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
CAGTTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA  
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
TCATTCCATGTTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA  
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTTCTTGCCTGGATC  
CATAGCGAGAGTGCTCTGTATTTTTTTTTTAAGATAATTGTATTTTTGCACACTGAGATATAA  
TAAAAGGTGTTTATCATAAAAA

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**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRALARRRKKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAGAACCATGAGGAAAAAATTGTATGAAAATGGTGT  
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC  
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAGAAGCGAAAAGGAAGGAACTTCAGTCAACATATTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA  
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTTGGAAATGGTCCTGTTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTTCGAACTGCCA  
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
AT**TAAA**ATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAA  
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
TTAA

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## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLLVSVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKLSEELLDKWSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAI CFLT TSEE VQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCTGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCTGTCACCGTCTTTGGGCTGAAA  
AAGAAACCCCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
ATTAAAAAAAAAAAAA



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## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACTATGTTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCACGGGTGC  
CCACTCAGGTCAC TTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC  
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

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## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT  
GACTCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
CGAACCACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCCGGACCTC  
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC  
TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG  
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC  
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC  
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA  
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAGCTT  
GCCCCGGGGCA

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## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA  
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG  
CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
GGCTGCGGCTGCCCACACGGCTCACCAATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTTCAGTTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTTACAGATTATTTGTG  
TGTGTCTGTTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCCTTTGGAATTAGTTTGTGTTGGTTCTTGTA  
AAAACCTTGGAATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA  
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC  
TCACTTTAATTAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT  
TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
TTAATATATGTTAAAAAA

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## **FIGURE 126**

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTCAGCCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA



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## **FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658  
><subunit 1 of 1, 257 aa, 1 stop  
><MW: 28472, pI: 9.33, NX(S/T): 0  
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGGLGF  
GIMSGVFSFVNTLSDSLPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLCQDKN  
FLLYNQSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTCTGGGCTTGCCCTTC  
 TTGGTGCTCTTGGTGCCCTCGGTGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGC  
 CGAGTTTGTAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGA  
 CCCGCAACAGGACAGAGGGCGTGCCTGTGTCTGTGAACGTCTTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTT  
 GTGGTCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTA  
 CCTCTACCAAAAAGTGAACGAACCCTGTGTGAGCCCCCACCAAGAATGAGTCGGAGATTCACTTCTTCTACG  
 TGGATGTGTCCACCCTGTCAACAGTCAACACCACATACCAGCTCCGGGTGAGCCGCATGGACGATTTTGTGCTC  
 AGGACTGGGGAGCAGTTTCACTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGG  
 CGTGGACTCGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTAGGATGTGC  
 TGTGTCTGTCTATGACCTGGACAACAACGTAGCTTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCC  
 ATCACCCTACAGCGCAAGACTTCCCCAGCAACAGCTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGC  
 CTGCGGGGGCTCCCTGCCTTCTACCCCTTCGCAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAAACCC  
 TGTGCTGCTGGTGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATATTT  
 CTCTCTTTTACCTGCTGACCGTCTCTCTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGAAGACCCCTGCTGGT  
 GGCCATTGACCGAGCCTGCCAGAAAGCGGTCAACCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCTT  
 ATGAGGGTTACAACATATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACT  
 GGGGACCTCTTACGGTTACAGGGCCGCTCCTTTGAACCTGTAGTACTCGGCCCGAGTGGACTCCATGAG  
 CTCTGTGGAGGAGGATGACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCAATTCGACCAAGCAAT  
 ACCTCTATGTGGCTGACCTGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAAC  
 ATTGCCACCATGTGTCTTCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGT  
 CACAGGGAATCAGGACATCTGCTACTACAACCTTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACA  
 ACATCTCAGCAACCTGGGGTACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAAC  
 CACAACCGGGCCCTGCTGCGCAATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTA  
 CGCCATGGGCACAGCCCTGATGATGGAGGGGCTGCTCAGTGCTTGCTATCATGTGTGCCCCAACTATACCAATT  
 TCCAGTTTGACACATCGTTTATGTACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCG  
 GACATCAACGCCAGCGCTACAGTGCCTACGCCTGCCTGGCCATTGTCTCTTCTCTGTGCTGGGCGTGGT  
 CTTTGGCAAGGGAACACGGCGTTCTGGATCGTCTTCTCCATCATTCACATCATCGCCACCCTGCTCCTCAGCA  
 CGCAGCTCTATTACATGGGCCGGTGGAACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACA  
 GACTGCATCCGGCAGTGCAGCGGGCGCTCTACGTGGACCGCATGGTGTGCTGGTTCATGGGCAACGTCTACAA  
 CTGGTGTGCTGGCTGCCTATGGGCTTATCATGCGCCCCAATGATTTTCTGCTTCTTGTGGCCATTGGCATCT  
 GCAACCTGCTCCTTTACTTTCGCTTCTACATCATGAAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCC  
 CTGCTCTGCATCGTTTGCACCTCCGTGGTCTGGGGCTTCGCGCTCTTCTTCTTCTCCAGGGACTCAGCACCTG  
 GCAGAAAACCCCTGCAGAGTGCAGGGAGCACAAACCGGGATGCACTCCTCCTCGACTTCTTTGACGACCAGACA  
 TCTGGCACTTCTCTCTCCTCATCGCCATGTTCCGGTCTTCTGCTGCTGACACTGGATGACGACCTGGAT  
 ACTGTGCAGCGGGACAAGATCTATGTCTTCTAGCAGGAGCTGGGCCCTTCGCTTACCTCAAGGGGGCCCTGAGC  
 TCCTTTGTGTCATAGACCGGTCACTCTGTGCTGTGTTGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATG  
 GCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCTGGGACAGCCATGGGGTGGCATGGAACCTTGACGTGCC  
 CTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCCAGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTG  
 GGGCCTTCCATGGGCCCCCTGTCTTTGGCTCTCCATTTGTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCT  
 CCCCATTTCATGCCTTGCATTTTGGCCGTCTCTCTCCCCACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTT  
 CCTCCCACTACTCCCACTCCAGGGCCTAGTCTGGGGCTGAATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTT  
 GGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCCAGGATGGATGGGGGTATGAGATTTTGGGGGTG  
 GCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGGCTGGGGCAGTGCATTTCTTCTTCCCTCTGAC  
 CTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATTTGAGAACCCTTCTGATTCAAGAGGCTGAA  
 TTCAGAGGTACCTCTTCTATCCCATCAGCTCCCAGACTGATGCCAGCACCAGGACTGGAGGGAGAAGCGCCTCA  
 CCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCAGCTGGTGGCCTTTTCACTGCCATTGACAC  
 TGCCCAAGAATGTCCAGGGGCAAGGAGGGATGATACAGAGTTTCAAGCCGTTCTGCCTCCACAGCTGTGGGCAC  
 CCCAGTGCCTACCTTAGAAAGGGCTTCAGGAAGGGATGTGCTGTTTCCCTCTACGTGCCAGTCTTAGCTCG  
 CTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGCTCTTCAAGCAAGTTCTGTGTTAGTCAAGCAGACA  
 TACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCACCTGGCCACCTGGTCTTGGATCC  
 CTTCTGCTCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGGCGGGGCTCTGCTTGGGGATGGG  
 AATGTGTTTTTCTCCCAACTTGTTTTTATAGCTCTGCTTGAAGGGCTGGGAGATGAGGTGGGTCTGGATCTTT  
 TCTCAGAGCGTCTCCATGCTATGTTGCAATTCGTTTCTATGAATGAATTTGCATTCAATAAACAACCAGAC  
 TCAAAAAAAAAAAAAA

## **FIGURE 130**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT  
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE  
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSEVI  
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV  
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLVLVSQAVTSEAYVSGMLFCLGIFLSFYLL  
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL  
VDSAGTGDLSYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL  
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYNFLCAHPLGN  
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGFLFYAMGTALM  
MEGLLSACYHVCPCNYTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS  
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYIMGRWKLD SGIFRRILHVLYTDCIRQCSG  
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI  
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRCILLDFFDDHDIWHFLSSIA  
MFGSFLVLLTLDDDLDTVQRDKIYVF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### **Leucine zipper pattern.**

amino acids 497-518

#### **N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTG  
 ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC  
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA  
 GGCAAGGCCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCTTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCTTCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC  
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAAC  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCCTGAGTTCATCACTTCCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGCCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTCTCTGTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC  
 GCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA  
 TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACTCTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC  
 GTGGAGGGGACAGTGCATGCGCAAGGTGGGGCCGATGAAGGGCATGCCACGAAGCTGTGGC  
 AGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCCTCATCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
 ACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTGTTGCCCAATAATAAAGCCCCA  
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPaelSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSpDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFevNAEGNLYVTRELDREAQAeyLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLsaEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAfQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTaIDADLEPAFRLMDFAIERGDTE  
GTFGLDWEpDSGHVRLRLCKNLSyEAAPsHEVVVVQSVAKLVGPgPGPGATATVTVLVERV  
MPPPKLDQESyEASVPISAPAGSfLLTIQPSDPIsRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIpVVVSHNAQMWQLLVRVIVCrcNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTTCAGTCTGCAGGCATTTAAATCCTTCCTG  
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTTGAC  
CTGGCGAGGAGGGTGAAGATTGGACATTTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
CAGCACTGGGAAAGGCGTGAGGCGGCCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG  
AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAATCC  
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGTCAGGAAAG  
GGAGCCAGCGACAACCCCTTGCTCCGAAGTGTAACCATGGACCCACGCCAATTCCGGAAGTGGA  
GGTGAAATCAGTGGTAGATTTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA  
GTACCAAGTGGGTCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
CGTATGACAACGGCATCAAATTTGCATTACATTTTGAGTTGAGAGATACCGGGACCTATGGC  
TTCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT  
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
CGTGTGTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG  
CTGTTTTTTGATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC  
AGCATCACCCCTTCCCTGGGTGGCATGTCTCTCTACCTCATTTTTTAGAACCAAAGAACATC  
TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTTT  
TCGCAGTCTTCCCTGGAATAATTTTCCCTTGAGCAGCAAATCTTGAGGGATATCAGTGAAG  
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTC  
CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA  
ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
TGCCGGGCCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC  
TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTGTATTTCAGTGTG  
ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA  
GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCCTAATGGGCTTACCTCCT  
CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT  
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCTGTGTT  
TCCTTGTCTGGTTTGT  
TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT  
GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCCTTTTGTGTGTGTGTGTGTGTGT  
TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

100

[illegible]



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## **FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESA IHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

**FIGURE 137**

•

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSA NTGSSV ISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVA AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNH GAPHRPRWSPNWFWR RPVSSI AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA

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## **FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

**FIGURE 141**

CTCGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGG  
 CCCCCGGGGGGCGATGACCGTGCCTGACCCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACT  
 CGGGGGCGGACCGCGGGGCGGAGCTGCCGCCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGACACC  
 GTCGCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCT  
 GCCGCTCGGCCACCGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGTCAGCCCGCCGCTCCGACCTGGGCGC  
 TCAGCCCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCC  
 AACTACACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACT  
 CAGTAGCAACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAAC  
 AGCAGTGCAGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAACTACATCAAGATCCTCTGCCGCTCAGC  
 GGCAGTCACCTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCAC  
 CCTGGCAAGGGACGAGAAGGGGAATGTCCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCA  
 AGTCCACTGCCCTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCC  
 ATCTCGCGGAGCCAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGT  
 GGCCTCAGCCTACATTCTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCG  
 AGACTGGCCAGGAATTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAG  
 GGTGGAGAGCGGGTGCTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGGGCCGACGA  
 TGGCTTCCCCCTTCAACGTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCCTT  
 TCTATGGGGTCTTCACTTCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTGTCTTACAATGAAG  
 GATGTGCAGAGAGTCTTACGCGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCA  
 CCGGTGCCACACCCCGCCTGGAGCGTGATACCAACAGTGCCCGGAAAGGAAGATCAACTCATCCCTGC  
 AGCTCCCAGACCGCGTGCTGAACTTCTCAAGGACCACTTCTGATGGACGGGCAGTCCGAAGCCGATGCTG  
 CTGCTGCAGCCCCAGGCTCGTACCAGCGCGTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGT  
 CCTCTTCTGGGCACTGGTGACGGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGTGCACATCATTGAGG  
 AGCTGCAGATCTTCTCATCGGGACAGCCCGTGAGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCG  
 GCCTCAACTCGGGCGTAGTCCAGGTGCCCATGGCCAAGTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCT  
 CGCCCGGACCCCTACTGTGCTTGGAGCGGCTCCAGCTGCAAGCACGTGACCTCTACCAGCCTCAGCTGGCCA  
 CCAGGCCGTGGATCCAGGACATCGAGGGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCCG  
 TCTTTTGTACCAACAGGGGAGAAGCCATGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTG  
 CCGCTCCTCTCAACCTGGCGACCCGACTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCC  
 ACGTGCTACCCACTGGGGACCTGCTGCTGGTGGGCACCCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAG  
 GAGGGCTTCCAGCAGCTGGTAGCCAGCTACTGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGA  
 GGGTGGCAGTGTACCCGTCATTATCAGCACATCGCGTGTGAGTGCACAGCTGGTGGCAAGGCCAGCTGGGGTG  
 CAGACAGGTCTACTGGAAGGAGTTCTGCTGATGTGACAGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTTA  
 TTCTTGCTCTACCGGCACCGGAACAGCATGAAAGTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGCACCCAA  
 GACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGCCACTCAACGGCCTAGGGCCCCCTAGACCCCGCTCGATC  
 ACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCGGGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTC  
 AGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTGTGCCCCCGGGCCCCGGTCCGCCTTGGCTCGGAGATCCG  
 TGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGCTGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGG  
 TCAACTGGACCTCCCCCTCGCTCTGCTCTTCTGTTGAACACGACCGTGGTGCCCGCCCTTGGGAGCCTTGGAGC  
 CAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCCTACCACCCAGACACCCAAACAGCCGTGGCCCCAGA  
 GGTCTGGCCAAATATGGGGGCCCTGCCCTAGGTTGGTGGAAACAGTGTCTCTTATGTAACTGAGCCCTTTGTTTA  
 AAAACAATTCCAAATGTGAACTAGAATGAGAGGGAAGAGATAGCATGGCATGCAGCACACAGGCTGCTCCA  
 GTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGGTTGTCTGAGACAGAGTTGGAACCCCTCACCA  
 CTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGCCCTGTCTCACTGCAGATTGAGACACAGCTTG  
 GGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTGTTGCTGCTGCCGTGCTCCACACCTCAGGGAC  
 CAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTCGGACCCAACTCCTGGACCTTTCCAGCCTG  
 TATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGATTTCTGTGACAATGTACGCCTTTCCCTCA  
 GAATTGAGGGAAGAGACTGTGCGCTGCCCTTCTCCGTTGTTGCGTGAGAACCCGTGTGCCCTTTCCACCATAT  
 CCACCTCGCTCCATCTTTGAACTCAAACACGAGGAATAACTGCACCTTGGTCTCTCCCCAGTCCCCAGTTT  
 ACCCTCATCCCTCACCTTCTTCACTTAAGGATATCAACACTGCCAGCACAGGGGCCCTGAATTTATGTG  
 GTTTTATACATTTTAAATAAGATGCACTTTATGTCAATTTTTAATAAAGTCTGAAGAATTACTGTTTAAAAA  
 AAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLTVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCF  
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP  
QLATRPWIIQDIEGASAKDLCSASSVSPSFVPTGKPCQVQFQPNNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVVIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCG  
AGCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCCGTCTGCGCCGT  
CGTGCCGGCCCCGCGTCCCCGCGCGCAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCCGCTAGCGCG  
CGCCGGGCATGGTCCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGC  
GGGGCCTGCGGGCGGCTCGGGGGCGCGATGGGCGCGGCGGGCCCGCGGCGGGCGGGCGCTGCCGGGCCGGG  
CCTCGCGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGC  
GGCGGGCGGGCGGCGGCGGCGGCCCGGCGGGCGGAGCGGCGCGGGCATGGCCCGCGCGCGGCCCGGCGCGCTGGCTC  
AGCGTGCTGCTCGGGCTCGTCTGGGCTTCTGTCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAA  
GCGAGCGGGCCACGGCGCCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGACAGGCGGCGGCTTCCAGGCGGGCG  
GGGCGCGCGGCGATGCGCGCGGGGCGCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGGCCCGCGCAGG  
AACTTTCTCTTCTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCCGCTACAGAACATG  
GTCCAAGACAATTCTGGGAAAGTTCACTTCTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAG  
TGCCACTACGGGGTGTGGACGACTCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGAC  
CACTACTTGGACAAGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAA  
CTTCTGAGGAGTTTGAACAGCAGCGAGCCCCCTTTCTTGGGCGAGACAGGCTGGGCACACGGAAGAAATGG  
GAAAACCTGGCCCTGGAGCCTGGTGAGAACTTCTGATGGGGGGCGCTGGCGTGATCATGAGCGGGGAGTGTCTT  
CGGAGAATGGTGCGCACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAG  
GTGTGTCCGGAGGTTTGCAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACG  
AGCAGAACAAAAGGGGTACATTAGAGATCTCCATAACAGTAAAATTACCAAGCTATCACATTACCCCCAAC  
AAAAACCCACCTTACAGTACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCAC  
AATACAGCTGCACCGCGAAATTGTCTGTATGAGCAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGC  
TGGGAATCCCTCCCTCCTTCATGAGTTTCAGCCCCCGCAGCGAGGAGATTCTGGAATGGGAGTTTCTGACT  
GGAAATACTTGTATTCCGGCAGTTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTT  
GGACGACATTGTATGCAGGTCATGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCA  
AAGAGATCCAGTACGGCTACCGCCGGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTG  
TACAAAAGCACAAAGGGAAGAAAATGACCGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAA  
AATCCAGTTTGTGGAGCATGAGGAGCTGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCT  
TGTCTTTCTCTCAAACCTCCCTGAAGAAGCTCGTCCCCCTTTCAGCTCCCTGGGTGGAAGAGTGAGCACAAAGAA  
CCCAAAGATAAAAAGATAAACATACTGATTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAAA  
CTTTGAGAAGACGTGTCTTATCCCAATCAGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACC  
CTGACAAGGCCAAACAAGTTGAACTGATGAGAGATTACCGCATTAAAGTACCCTAAAGCCGACATGCAGATTTTG  
CCTGTGTCTGGAGAGTTTTCAGAGCCCTGGCCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCT  
CTTCTTCTGCGCAGCTCGACCTCGTGTCTTACTACAGAAATCCTTCAGCGATGTGAGCAAAATACAGTTCTGGGCC  
AACAAATATATTTTCCAATCATCTTCAGCCAGTATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGAC  
AACCATTTTGCCTTTACTCAGAAAACCTGGCTTCTGGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGG  
AGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCATCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACA  
AGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCCAGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTT  
TGTGATCCCAATCTTGACCCCAACAGTACAAATGTCTTGGGTCCTGAGCATCGACATAGGTTCCAGCCCA  
GCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAAGTTACAGTAAAAGCAGCAATAAATGGCTCAGTGA  
GGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTTTAATTATCTAATTTATTTTCAAAAATTTTTTGTA  
TGATCAGTTTTTTGAAGTCCGTATACAAGGATATATTTTACAAGTGGTTTTCTTACATAGGACTCCTTTAAGATT  
GAGCTTTCTGAACAAGAAGGTGATCAGTGTTCCTTTGAACACATCTTCTGTGTAACATTATGTAGCAGACC  
TGCTTAACCTTTGACTTGAAATGTACCTGATGAACAAAACCTTTTTTAAAAAATGTTTTCTTTTGAGACCCCTTG  
CTCCAGTCTATGGCAGAAAACGTGAACATTCCTGCAAAAGTATTATTGTAACAAAACACTGTAACCTCGGTAAA  
TGTTCTGTGTGATTGTTAACATTCCACAGATTCTACCTTTTGTGTTTTTTTTTTTTTTTACAATTGTTTTTA  
AAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATAGCTGTTTCATCATTGTCTTCAGGAGAGCT  
TTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGCCACGTAGGTTTTTTGTTTGTGTTTTGTTTT  
GTTCTTTTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATGCAGTGGCGCAATCTTGGCTCACTTTAA  
CCTCCACTTCCCTGGTTCAAGCAATTCCTTGCCTTTGCCTCCCGAGTAGCTGGGATTACAGGCACACACCACC  
ACGCCAGNAGTTTTTTTGTATTTTTTAGTAGAGACGGGTTTTCCACATGCAAGCCGAGTGGCCACGTAGGTT  
TTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGTATGTGGCTGTTCTCGTGGTAGTTCAATTCGGCCTAAATAG  
ACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTCTTCTTGACCCTTCTCTTTAAAGGGTAAAATATTAA  
TGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACTGAAACATACACACATACACCCT  
AATCAAAACGTTGGGGAAAATGTATTTGGTTTTGTTCTTTTCATCCTGTCTGTGTTATGTGGGTGGAGATGGT  
TTTCATTCTTTTCACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAATTTATTTAATATCTGTTGTT  
CAGAGCTCGCCATTTCTTGAGTACCTGTAGTTAGTATTATTATGTGTATCGGGAGTGTGTTAGTCTGTTT  
TATTGTGCAATAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTTCCCCTCC



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**FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGG  
GGACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTG  
TTTTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAA  
TAGCCTGATGCTCATTTGGAAAAATAAACCAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCT  
CATTATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

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## **FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNP MYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFFSKIQFVEHEELDAQELAKR  
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEVDL FNKVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC  
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAAACACACGGAAAGTACCCC  
ATTCTGGTTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAAAGTCACCTGTCAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTATTAAACAATAATATAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAAATAAAATTTTGGTTCAGGAAAAAA

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## **FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA  
GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG  
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTAC  
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC  
CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
AGACGTTTTTCCAGCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG  
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG  
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA  
GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTCTGGGGATGAGACAGAGAAGACCCTG  
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCCGACAGGTGGC  
CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC  
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTCTGCCTCACAGGTGAAGATTAAAGAGA  
CAACGAATGTGAATCATGCTTGCAGGTTTGGAGGCACAGTGTTTGCTAATGATGTGTTTTTA  
TATTATACATTTTCCCACCATAAACTCTGTTTGTCTTATTCCACATTAATTTACTTTTCTCTA  
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG  
AAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
TTCTAAATAAAATTTTAAACAAATTAACTAAACAATATTTTAAAGATGATATATACTACT  
CAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT  
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

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## **FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDGRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSIIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAAGAAGACCTACAA  
TACTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
AGTGTTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA  
GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGAGGACAG  
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
GAACCCTGCCAGATGGACTGCTTCCCTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCT  
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
TGTTTGCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
CCAGATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC  
TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
AGCTCCTCTCATTTTCAAGCAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA  
TAAGAAGAAAAAAATCCCCACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
TCCTTATTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
ACCTATAATAATTATACAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAATAT  
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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## **FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYTNVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)



**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCTCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCCGCACTCTGGTCCACGC  
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCCGAGCCGCAGGGGCGCTCTGA  
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA  
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPGLSSPAQPPDPPrMGevRIAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA  
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVpQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTLvhAAVGvGTALALLScaALVWHfCLrDRWGcPRRAAARAAGAL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGG  
CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
TTCTCCCTTACGGGGCTCACAATGGCCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA  
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGGTAGAGGAAGCAGTC  
ATTTTGACTTACTTTCTGTGGTTCATCCGGTCACTGATTGCTGTTTGCTGTTTCCCTTATCAT  
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT  
TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
GAACCTTATGGTTCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA  
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGT  
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAACAACCTGC  
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC  
CTTGAAGAATGACAACTCTCAGCACCTGTCACTGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
GAGTTATAAAAAGAAATGTACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT  
TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC  
CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTC  
CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
ACTTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTC  
AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA  
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
TCTGTATAAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA  
CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAATG  
AAGACTCTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAT  
GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA  
ATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAAGAGTATAGTATATTTATTT  
GAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTATTTTGTATTATTCTCAGAATATGGAA  
AGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

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## **FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLALLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTCLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG  
TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
TGTGTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGGCCCTGTC  
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT  
GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTCAGCATCCAGTACGA  
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTTCACGGCAGCCCCACT  
GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC  
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCCAA  
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTCTCAGGCACAGTCAGGC  
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
GGGCCCCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTCAGTGCTGGGAGCCGCTTCCTTCCTG  
CCCTGCCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC  
CTCTGCCCCACAGCCTCAGCATTTCTTGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  
TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
GGAACTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA  
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
CTGGCAAAAAAAAAAAAA

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## **FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF  
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNWF  
SACFDNFTEALAETACRQMGYSRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSL  
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWLTAAHCFRKHTDV  
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD  
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNAD DAYQGEVTEKMMCAGIPE  
GGVDTCCQD SGGPLMYQSDQWHVVGIVSWG YGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCA  
 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCCTCCTGGG  
 CCTTTTCCTCTTCCAAGTCTTCAAGTCTGTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCATGC  
 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTT  
 GACACTCTGCTCCTGAGTGGTGATGGAATACTCTTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATAT  
 CCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTG  
 CCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTCACCCAT  
 CTCTACACCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCCTACCTGTTGCC  
 CATCTCGGAGGACAAGGTCTAGGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCT  
 TGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTG  
 GGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCAT  
 CCCTTCGACCCAGGTCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA  
 CATCGCGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC  
 CTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTTCATCCGCCACGCGGTCTGTCTCC  
 CGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCT  
 CTGCGGTTTGTGCCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA  
 ACTTCACGCTGGACTACTTATAGGGGGCCCTGAGACCAACCCCCCGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTC  
 TGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGA  
 AATCTGGCGTGGAGTATACACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCTAG  
 TACCTGGGAACCACACAGGGTCTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAAG  
 GATTGAGCTGTTCCCTGACCTGAACCTGTTTCGAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAG  
 GCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTT  
 GCCCCGGACCCCCACTGTGCTGGCTGGGACCCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACCTC  
 CTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCCTTCGGC  
 CTGAGAGCCCCCGCAAATCATTAAGAAGTCTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCCTGCCCCAC  
 CTGTGACGCTTGGCCTCTTATTATTGGAGTCTAGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAA  
 TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAGTGTGGGCAACTGAGAATGGCTTTT  
 CATAACCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAACTGGCAGGCATC  
 CCCCCGGAGCATGTGAAGGTCCCGTTGACCAGGGTCACTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTG  
 GCCCCACTTTGTCACTGTCACTGTCTCTTTGCCCTTAGTGCTTTAGGAGCCCTCATCATCTCGTGGCCTCCC  
 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTA  
 AGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACCTG  
 CCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGG  
 GCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTG  
 CTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTAC  
 CAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGA  
 GAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTCCAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGC  
 CTGTCCCAGGACCCCTATGGTAATGAACACCAACATCTAACAATCATATGCTAACATGCCACTCCTGGAACT  
 CCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCACTGCAGGGATCTGCTCCCTCCTGC  
 TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTGCTTCA  
 GTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACC  
 CTAGCTGACCCCTTACCTCTCCCCCTCCCTTTTCTTTGTTTTGGGATTGAGAAAAGTCTTGTGAGAGACTG  
 TTTATTTTTTTATTAAAAATATAAGGCTTAAAAAAA

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## **FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ  
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE  
ETASEFDDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN  
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVLFLVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVDADNNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704





## **FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
 CATTCTTTCACCTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTC  
 CAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCAATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA  
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCAAGTGTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGTGGA  
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCG  
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTTTACAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACATTAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
 CTTGTCCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA  
 TCACACCCTGACTCTTCCAGCCTCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTTCAAGTTTCTGTTT  
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGC  
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGTTTTCCAGATTTCTTGAAAAATAAAAGTTTACA  
 GCGTTATCTCTCCCAACCTCACTAA

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPKPFVAILSTSFGSLEFGLPIPLSYVPV  
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF  
INSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVIWKCQCShWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIQHGVPVMGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQYLFDFVFVLLGLT  
LGT LWLCGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT  
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC  
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA  
AGACCGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC  
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCTGTCTGGAGGGGGAGTGCCTGGTGGTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
GAGTGGCATTGTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTCGTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC  
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA  
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCCCTCATCTTCCCTCTCT**G**AGGACCCAAAGTCTTTCAAGCACAGAAT  
CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCCACTCTTTGCATGGGACCCTGTGCCAAACACCCAAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCCAGTTACC  
CTCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCT  
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG  
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCTCCCAGCTCTC  
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT  
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTATTACCTGGGATTCCATGATTATTCCTT  
CAGACCCTCTCCTGCCAGTATGCTAAACCCTCCCTCTCTCTTCTTATCCCGCTGTCCCAT  
GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT  
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA  
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

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## **FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32

**FIGURE 163**

[illegible]

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## **FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWLVFDWNTPKKGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKFGLPETEVLEVN

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCCGGGGCGGGCGGCGCGCACTCGCTGAGGCCCGACGCGAGGGCCGGGCGGGCCC  
 AGGGCCGAGGAGCGCGCGGCCAGAGCGGGGCCGGAGGCGACGCCGGGGACGCCGCGGACGAGCAGGTGG  
 CGGCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTT  
 GGACGGCTGTCTCAGCGAGGGGCCGTGCACCCGCTCCTGAGCAGCGCCATGGGCTGCTGGCCTTCTGAAGA  
 CCCAGTTCGTGCTGCACCTGCTGGTGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTG  
 TGCACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTG  
 GAGCCAAGTGGTCATGCTGCTGGAGTGGTGGTCTGACCGAGTGTAAGTGTTCACGGACCAGGCCACGGTAG  
 AGCGCTTTGGGAAGGAGCAGCAGTCATCATCTCAACCACAAGTTCGAGATCGACTTCCTCTGTGGTGGACC  
 ATGTGTGAGCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCAT  
 CGGCTGGACGTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCG  
 AAGGGCTGAGGCGCCTGTGCGACTACCCCGAGTACATGTGGTTTTCTCCTGTACTGCGAGGGGACGCGCTTCACG  
 GAGACCAAGCACCAGCTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCC  
 GCGGACCAAGGGCTTACCACCGCAGTCAAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGA  
 ACTTCAGAGGAAACAAGAACCCTGCTCGGTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTG  
 AGGAGATTTCTCTGGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGA  
 GAAGGACGCGCTCCAGGAGATATATAATCAGAAGGGCATGTTTCAGGGGAGCAGTTTAAGCCTGCCCGGAGGC  
 CGTGGACCCTCCTGAACCTTCTGTCTGGGCCACCATTCCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTC  
 TTTGCCAGCGGATCACCTCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGAG  
 ACTGATAGGAGAATCGCTTGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCC  
 TAGGCAACAGAGCAAGACTCAGTCTCAAAAAAAAAAAAAAAAAACAAAAAATTCGGAGTTGAAGCTG  
 TGTAGTTACTGACATGAAAAATTCAGTAGAGGCTGAACAGCAGATTGAGCAGGCAGAAAAAATCAGCAAGCT  
 TGAAGATGGTACCTTGAGATTTTTCAGGCTAATGAAAAAGAATGAAGGAAAAATTAACAGCCTCAGAGACCCAT  
 GGTGCACCGTCACACAAATCAACATATGCATGATGAGAGTCCAGAAAGGAGAGAGAAAGGGTCAGAAAGAA  
 TGGCCACAAGCTGATGAAAAACAGTAACCTACCCACTCAGGAAGCTCAGTGAAGTCCAATGAGGATGAATATCA  
 GAGATCCACACCTAGATATTTTATAATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCA  
 ACTTATCTTTGTTCAAAGGATCTTTGATCAGATTAACAGCTCATTCTCTCAGAAATCATGGGAGCCAGGAGAT  
 AGTGGGATGAACACTGTTGAAGGCAAAACCTTCAACTGTAATTATTGGACTTTTGTAGTCTTAGATGGTCCCTGAC  
 CTCTTTGTCTTCAGGGACAGTTTTTCAATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAA  
 GGCCTGTCTTTAGGCCGGGCACAGTGGCTTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATC  
 ATTTGGGGTCAGGCTGATCTCAAACCTCTGAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTGTGAT  
 TGCAGGCGTGAGCCACTGCGCCTGGCCGGAATTTCTTTTAAAGGCTGAATGATGGGGGCCAGGCACGATGGCTC  
 ACGCCTGTGATCCCAAGTAGCTTGGATTGTAAACATGCACCACCATGCCTGGCTAATTTTGTATTTTAGTAG  
 AGACGTGTTAGCCAGGCTGGTCTCGATCTCCTGACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGG  
 ATTACAGGCGTGAGCCACTGTGCCTGGCCTTGAGCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTA  
 TCTTCTTTGGGGAATGTCTGTTCAAGTCCTTTGCCTTTTTAAATTTTTATTATTTATTTATTTATTTTGT  
 AGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTACAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCT  
 GGGCTGCAGTGATCCTCCACCTCAGCCTCCCTGTAGCTGATTTTGTATTTTGTATTTTGTAGCTGTAG  
 TTTTGTATTTTTTGTGGAGACAGCATTTACCATGATGCCAGGCTGGTCTTGAACCTGAGCTCAAGTGAT  
 CTGCCTGCTTCAGCCTCCCAAAGTGTGGGATTACAGACATGAGCCACTGCACCTGGCAAACTCCCAAATTC  
 ACACACACACAAAAAACCTGATTCAAATGGGCAGAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGAC  
 TGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTGCAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCC  
 TGGACAACAGAGTGAGACCCTGTCTC

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## **FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLV  
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLLNFRGNKNPSLLGILYGKK  
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
FLSWATILLSPLFSFVLGVFASGSPLLILTLFLGVGAASFGVRRRLIGESLEPGRWRLQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

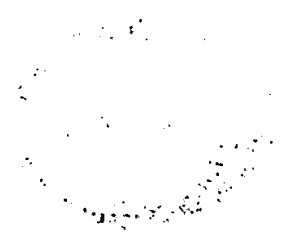
**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



**FIGURE 167**

GATATTCTTTATTTTTAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTGCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAATGCTCTCATAAGACCCTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCAGTAGGCCCCAGGTGGGCATCTCTAACAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

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## **FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCFSSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR  
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAAATCTGTTTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT  
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGG  
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT  
CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAGGC  
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTTCCGCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
TCCAAACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

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## **FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCCTCCTGCCCCGCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
CCTGAGTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

### FIGURE 173

CCGCGCCGCGCAGCCGCTACCGCCGCTGCAGCCGCTTTCGCGGCGCTGGGCCTCTCGCCGCTCA  
GCATGCCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCCTCAC  
TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCC  
CATCTTTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTACG  
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG  
GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCCGACAG  
CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG  
GGGTCATGGCCGTCACAGCGGTAAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC  
GGTCTCGAAACGAGCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
AAGAGGAGAAGCTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCCAGGACTTCACACCT  
GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGGACGGAAAAAAAAGAA  
GGCGCCGTCAGCTCCGACTCCGACTCCAAGGCCGATTTCGGACGGGGCCAAGCCTGAGCCGG  
TGGCCATGGCGCGGTTCGGCGTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG  
TCTGTGAAGAAGCCTCCGAGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG  
GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
TGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGG  
CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA  
GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGCAGCGGCGGCAGCAGCGGGG  
ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT  
CCCCCGTCCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
GAAGAAGCCGCAGTCCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT  
GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGT  
GCCTGAATGCCCTAGAGGAGCTGGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAGAAC  
ACAGACGTGGTGGCCACCTTGAAGAAGATTTCGCCGTTACAAAGCGAAACAAGGACGTAATGGA  
GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGG  
TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG  
GAGCTGGCCGGGGAGGAGGCCCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCACCGATCTCTC  
AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG  
AGGAGGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC  
GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG  
GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCGGGCAGCCAGGCCCCAGCCCCCGC  
CCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACTGTGGG  
GAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTTTTTTTTTCTGCCTAATTTCTGTGATT  
TCCAACCAACATGAAATGACTATAAACGGTTTTTTTTTAATGA

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## **FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFFGTHETAFLGPKDLFPYD  
KCKDKYGGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQKPVKVERTKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEKDPSTDLSAPVNGEATSQKGESEAEKHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13



**FIGURE 175**

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAT  
 AACACCATTGAAAGAGAACATTGTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAA  
 GATTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCATTGAA  
 GCAAAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATCCCTTTTTGGGTT  
 CATCAGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGAC  
 CACATCTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACG  
 GGTGGAATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTATCAGAGTACTTCAGCCCT  
 ATAACAAAACCTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTC  
 TACAAGGAGGATATTATATTCAAACCTAGACACACATAAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCC  
 TCAGCAGCCTTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAG  
 ATACTGCATTCACTCGATCCCTTGGGCCTACTCATGACCACCTACATCAGAACTGACATTTAGAGCACTAC  
 TGGCTCAATGGAGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATA  
 TTTCTTCTTTCTGTAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTT  
 GTAAGAATGATGTAGGAGGACAACGCAGCCTGATAACAAGTGGACGACTTTTCTTAAGGCCAGCTGATTTCG  
 TCAATTCCTGGAAGTATGGGGCAGATACCTTTTGTATGAGCTTCAAGATATTTATTACTCCCAAGAGAGA  
 TGAAAGAAATCCTGTAGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGT  
 ATAGCATGGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTG  
 CAGTATGATGGGAGAATTCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTC  
 CACCCGAGATTTTCCAGATGATGTCTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAG  
 TTGCAGGAGGACCAACGTTCAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGATCATGTTCATT  
 GCAGAAGATGGCCAGTACGATGTAATGTTTCTTGGAAACAGACATTGGAAGTCTCCTCAAAGTTGTCAGCATTTTC  
 AAAGGAAAAGTGAATATGGAAGAGGTAGTGTCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGA  
 ACATGGAATTGTCTCTGAAGCAGCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCAGCTCTCCTTGCAC  
 AGATGCGACACTTATGGGAAAGCTTGGCGAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAAA  
 TGCATGCTCTCGATATGCTCCTACTTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCA  
 CCCAGTCTGGGACATCGAAGACAGCATTAGTTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTTGAATTT  
 AACTCAACCTTTCTGGAATGTATACCTAAATCCCAACAAGCACTATTAAATGGTATATCCAGAGGTGAGGGGA  
 TGAGCATCGAGAGGAGTTGAAGCCGATGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGC  
 AGAAGAAGGATTCTGGGATGTATTACTGCAAGGCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACT  
 TTGAATGTCAATTGAGAATGAACAGATGGAAAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCT  
 ATTGGCTGAGTCACGGTTGAGATACAAAGACTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCACT  
 ACTGCGAACAGATGTGGCACAGGGGAGAAGCGGAGACAGAGAACAAGGGGGGCCAAAGTGGGAAGCAGATGCAG  
 GAAATGAAGAAGAAACGAAATCGAAGACATCACAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTT  
 TTCTACTTAATTTAAAGAAAAGAATTCCTTACCTATAAAAAACATTGCCTTCTGTTTGTATATCCCTTATAGTA  
 ATTATATAAATGCTTCCCATGGAGTTTGTCTAAGGCACAAGACAATAATCTGAATAAGACAATATGTGATGAATA  
 TAAGAAAGGGCAAAAAATTCATTTGAACCAGTTTCCCAAGAACAAATCTTGACACAAGCAAAGTATAAGAAATAT  
 CCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTATGTTTTGAGTTTTGGAATTTATTGTCATGTAATAGTT  
 GAGCTAAGCAAGCCCCGAATTTGATAGTGATATAAGGTGCTTTATTCCCTCGAATGTCCATTAAAGCATGGAATTT  
 ACCATGCAGTTGTGCTATGTTCTTATGAACAGATATATCATTCTATTGAGAACCAGCTACCTTGTGGTAGGGA  
 ATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATCAACAGGAACCTTCTCAGTGAGCCATTCACTCCTGG  
 AGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTCTGGCCACTGGGGTTAAATTTAGTGTACTACAACA  
 TTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCTATTGACTAGTCAGGAGTAACAGGTTTACAGAGA  
 GAAGTTGGTGCTTAGTTATGTGTTTTTAGAGTATATACTAAGCTCTACAGGGACAGAATGCTTAATAAATACT  
 TTAATAAGATATGGGAAAATATTTTAATAAAAAAGGAAAAACATAATGATGTATAATGCATCCTGATGGGAAGG  
 CATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCATAAATTTCTGGCTTTGGGGAAAACCTCATATCC  
 CCATGAAAAGGAAGAACAAATCACAAATAAAGTGAGAGTAATGTAATGGAGCTCTTTTCACTAGGGTATAAGTAG  
 CTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACAACTGCTAGCAAAATCTGAGGAAACATA  
 AATTCCTCTGAAGAATCATAGGAAGAGTAGACATTTATTTATAACCAATGATATTTTCAAGTATATATTTCTCT  
 CTTTAAAAAATATTTATCATACTCTGTATATTTCTTTTACTGCTTTATTTCTCTCTGTATATTTGGATT  
 TTGTGATTATATTTGAGTGAATAGGAGAAAAACATATATAACACACAGAGAATTAAGAAAAATGACATTTCTGGG  
 GAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAATTTTAAACAACGGAAAGGGTTAAATTAACCTCT  
 TTGACATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAATTGTAGTATGTTTTTGAATTTAA  
 CAATAAATAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL  
 GSSEGLDFQTLTLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGvyKEDIIFKLDTHNLESGRLKCPFD  
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNgaKFIGTFF  
 IPDTYNPDDDKIYFFFRessSQEGSTSDKTILSRVGRVCKNDVGGQrSLINKWTTFLKARLIC  
 SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTTSSIFKGSaVCVYSMADIRAVFNGP  
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
 AGGPtFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVsisKEKWNMEEVVLEE  
 LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYgKACADCClARDPYCAWDGNA  
 CSRYAPtSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIvFGIEFNSTFLECIPKSQQA  
 TIKWYIQRSgDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYyCKAQEHtFIHTIVKLTLN  
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
 KGGPKWKHMqEMKKKRNRRRHrdLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACC GCGGGGAGCAG  
 ACAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTCCCCACCCC  
 ACCTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCA  
 AGAGTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGG  
 CATCGGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGGAT  
 CTTGGAGCCATTGAGGGTGTCTGAGGCTACAGAGGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAAT  
 AGTTAAGAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCCTAGTTCTGTAGC  
 CCCAGGTAAGGGAGTGA CTTAACCTCTCTGGACTTCAATTTCTCTATCACTAAAGTAGGGCCAATAATAGCACC  
 CACCTCATAGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCAT  
 GCCCCACAGTATTTCCACCCACCCCTGTTCTCTGCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGG  
 CAGCAGGCTTCAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGC  
 ACAGGTGAGCCAGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGC  
 TGAAGCCAGCCATGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCAG  
 AGGGACCTCTCTCAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTT  
 TGAGGAGCTGCCCCCAAGCCCTGGCCACGAGGGCCCTCCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGG  
 CAGGGCGTGAGGATGAGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAA  
 TGGGTCAAGGCTCGGAACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTC  
 CCTCCAGAGAGCAGCCAAGACAGTGACAATCCCTGCGGGGCAGAGCCCACAGCATTCCTGGCACAGGCCCTGT  
 ACAGCTACACCGGACAGAGTGACAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGCC  
 CAAGATGGAGTAGATGACGGCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCCCTCCCTGCTGGT  
 GGAAGAGCTGCTTGGCCCCCAGGGCCACCTGAACTCTTGACCTGAACAGATGCTGCCGTCCCCTTCTCCTC  
 CCAGCTTCTCCCCACCTGCACCTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCC  
 CTGGA CTTCCCTGGGTTCTTGACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGC  
 TAAAGCCCCGGATCCTGGCCACCCAGATCCCCTCACCTGGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGC  
 TGTCCCTATCTTCAAGCTGTGACACCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCT  
 TATTTCCACCCTCACCTCCAAGGGTGGAACTTGCCCCCTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTT  
 CCAAGAGCTGCTTATCATCTTAGGACCGGAACACTACCTTCTCTTCTGTCTATGACCTATCTAGGGTGGTGAA  
 TGCCTGAAATCTCTGGGGCTGGAAACCATCAAGGCTCTCTAGTAGTTCTGGCCCCCTCTTCCCCACCT  
 GGCTCCATGACCCACCCCACTCTGGATGCCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAA  
 TCAGGAGCTGGAGCCAGGATGCGAAGCAGCTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGC  
 AAGGCCAGGCCAGGGCCTGGGCCTCTTGTGCTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCCA  
 CCACGGGCAGGGCCTGCTCCCAGCTGCCACGCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGAGGC  
 AGCCTGTTGCAGGCAGGGGAAGGAGAAGAGACTGAGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTG  
 TGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTCAGCTGGGGGGCAGTGCTGTCCAGTGAGGGGGAGGGCTTTCA  
 CGCCACCCACCCCTGGCCCTGCCAGCTGGTAGTCCATCAGCACAAATGAAGGAGACTTGAGAGAAGAGGAAGAA  
 TAACACTGTTGCTTCCCTGTTCAAGCTGTGTCCAGCTTTCCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCA  
 CCAAACCAAGGGATTTATAGCAAAGGCTAAGCCTGCAGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAA  
 TAGTTTAAGTAGGTGATGGGAAGATGAGATTACCTCATTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTG  
 CTCCTGTGGTAGAGACCTGAGAGAAAGGGGAGGGGTCAACAATGAGAGACCAGGAGTAGGTCCTATCAGTG  
 CCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGCACTCCCGCTGTGTTTTCTACCTGGTGATCAGAA  
 GTGTCTGGTTTGCTTGGCTGCCATTTGCCCTCTGAGTGGGCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCT  
 CAGTGTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTGACAGGGGTTAGGCTGCTGTCCCTGAGTCCTC  
 CATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCCTCTCAGGGGGCAGCCTCTCCATGGCAGGCATC  
 CTGCTTGGGCTGCCCTCCCCAGACCCCTGACCAACCCCTGGGTCCTGTCCCCCACCAGAGCCCCAGCTCCT  
 GTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATACGCTTCTCAATGTGTGTCAACCGAACCTGGGAG  
 GGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTGGCCCTCCCCCTCTGACCAGGGACATCTGA  
 GTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTCAGATTGTGGGGCACATTGTGTAGCCTGA  
 CTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCCACTTTTGGGATCAGGTGCCTGATCACTGGGC  
 CCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCACAGAGAACACAGTGGTCTCCCCCTGTC  
 CCGGGGCGGCTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAGGCCTTCTGCTGCGGCTGCAATGGAT  
 GCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGAGGGGGCTCCGTCCTGCAGGCTGGAGGTGGCAT  
 CCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCTTCATGTTTTGTTTCTTACGTTCT  
 TTCAGCATGCTCCTTAAAACCCAGAACCCCAATTTCCCCAAGCCCCATTTTTTCTTGTCTTTATCTAATAAA  
 CTAATATTAAG

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## **FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSLPRESSQSDSNPCGAEPFAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPPELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGA  
AGAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGTCCCTACAGAGGGAGAGGCCAGAGAAGCTGCA  
GAAGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCC  
TGGGCACCTCTCCCAAGCCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCCTCAGCCCTTCTGAAAACCTT  
TGCCTCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGAC  
TTGGTGCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCCAGACAGGCTCGCATCCCCGG  
GAGGGGCTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGC  
TGGTGTGGCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAG  
GAGGAGATCGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTG  
CCGCTTGCAGGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGA  
CAGTGCAGTACCTGGGCCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATC  
AATGGAGATCCGGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAAATATCGGGG  
GGCTGAACCTCCACTCCAGCCCCCTGGAGGGAGGCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTAC  
GCCGGAAGAGTCTGCCAGCGGTCAAGGTCCCATGTGCAACGCTCAAGGCTCCTCTTGAAGAGCCAGCCCCAGA  
CCCCGAAGAGCCAAGCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGC  
CGCATTCACGGTGCAGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTCAAGCACC  
CAAGCATCCGCAATCCTGTGAGCTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAA  
GTGGGGCCAGTGCTGCCAGACCCCTGCGCAGCTTCTGTGCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTC  
GGGCCCTGACCCTTTGACACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGGCAGACGC  
TGGGTATGGCTGATGTGGGCACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAG  
TCAGCCTTCACTGCTGCTCATGAAGTGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAG  
TTTGAATGGGCCTTTGAGCACCTCTCGCCATGTCATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCT  
GGTCCCCCTGCAGTGCCCGCTTTCATCACTGACTTCTCGGACAATGGCTATGGGCACCTGTCTCTTAGACAAACCA  
GAGGCTCCATTGCATCTGCCCTGTGACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTT  
CGGGCCCGACTCACGCCATTGTCCACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTTGCCACCTCAATG  
GCCATGCCATGTGCCAGACCAAACACTCGCCCTGGGCGGCTGAGGACACCCCTGCGGGCCCGCACAGGCTGCATG  
GGTGGTGCCTGCCATGGACAGCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGG  
ACCATGGGGTGACTGCTCTCGGACCTGTGGGGGTGGTGTCCAGTTCTCCTCCGAGACTGCACGAGGCCTGTCC  
CCCGGAATGGTGGCAAGTACTGTGAGGGCGCCGTAACCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACT  
GGCTCAGCCCTGACCTTCCGCGAGGAGCAGTGTGCTGCCTACAACACCGCACCGACCTCTTCAAGAGCTTCCC  
AGGGCCCATGGACTGGGTTTCTCGCTACACAGGCGTGGCCCCCAGGACCAAGTGCACCACTCACTGCCAGGCC  
GGGCACTGGGCTACTACTATGTGCTGGAGCCACGGGTGGTAGATGGGACCCCTGTTCGCCGACAGTCTCCTCG  
GTCTGTGTCCAGGCGCGATGCATCCATGCTGGCTGTGATCGCATCATTGGCTCCAAGAAGAAGTTTGACAAGTG  
CATGGTGTGCGGAGGGGACGGTTCTGGTTGCAGCAAGCAGTCAAGGCTCCTTCAAGAAATTCAGGTACGGATACA  
ACAATGTGGTCACTATCCCCCGGGGGGCCACCCACATTTCTGTCCGGCAGCAGGGAAACCTGGCCACCGGAGC  
ATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTATGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCAC  
AGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTACAGCGGGGCCACTGCAGCCTCAGACAGCTGCAGGCC  
ATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTAGTGGCTGGCAACCCCCAGGACACAGCCTCCGATAC  
AGCTTCTTCGTGCCCCGGCCGACCCCTTCAACGCCACGCCCCACTCCCAGGACTGGCTGCACCGAAGAGCACA  
GATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAGGAAATTAACCTCACTATCCCGGCTGCCCTTCTGGG  
CACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTTCTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAG  
GGGCTGTGGGCGTGAGACCTGCCCTCCTCTGCCCCTAATGCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCT  
GGGAGGCAGTGATGGGTTAGTGGATGGAAGGGGCTGACAGACAGCCCTCCATCTAAACTGCCCCCTCTGCCCTG  
CGGGTCAAGGAGGGAGGGGAAGGCAGGGAGGGCCCTGGGCCCCAGTTGTATTTATTTAGTATTTTCACTTT  
TATTTAGCACCAGGGAAGGGGACAAGGACTAGGGTCTTGGGAACCTGACCCCTGACCCCTCATAGCCCTCACC  
CTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTGTGTGTATGCGTGTGTGTGTGTGTGAAA  
ATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTCCTTCTTCTGAATTTTATTTTTTGGGAAAAGA  
AAAGTCAAGGGTAGGGTGGGCTTCAAGGAGTAGGGATTATCTTTTTTTTTTTTTCTTTCTTTCTTTCTTTT  
TTTTTTTGGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATGGCACAATCTCGGCTCACTGCATCCTC  
CGCCTCCCGGGTTCAAGTGATTCTCATGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCTCCTGCCACCAACGC  
CCAGCTAATTTTGTTTTGTGTTTGGAGACAGAGTCTCGCTATTGTACCAGGGCTGGAATGATTTAGCT  
CACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGATTATAGGCAC  
TACCACCAACGCCCCGCTAATTTTGTATTTTGTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCG  
AACTCCTGACCTTAGGTGATCCACTCGCCTCATCCCAAAGTGCTGGGATTACAGGCGTGAGCCAGCCGTCGCC  
TGGCCACGCCCCAATAATTTTGTATTTTGTATAGTAGACAGGGTTTACCATGTTGGCCAGGCTGCTCTGAAC  
TCCTGACCTCAGGTAATCGACCTGCCTCGGCCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCAACGCCCCG  
TACATATTTTTTAAATTGAATTCTACTATTTATGTGATCCTTTTGGAGTCAGACAG



**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
 FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP  
 GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP  
 ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA  
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF  
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHAHELGHVFNMLHD  
 NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG  
 PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVPRNGGKY  
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK  
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL  
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
 PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152,  
 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560,  
 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT  
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA



**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILVLFWGSKHFWPEVPPKAY  
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI  
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPMLDERGYCCICYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
GCGCCTGCGCCGTTCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA  
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
GGCACCTTGCTTTGCCTGTCTTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTG  
GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
CCTGGCACCAAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA  
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA  
TTTCCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG  
TCCTCTTTCTGTGCGGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
ACTAATTCTTTAA

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## **FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCAATGCCTCAGTGG  
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC  
CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA  
CTGTTCTTAAGTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAAGCAGAAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAGCATCTACTCTTTTTTATCATTTACTTCAAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA  
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
TTCTTGTTGATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTGTACCATTTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAATTTGATGAACTGACAATCCAATTTGA  
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCTACCTCTGGGA  
TTGTCTTTGTTCATCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT  
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGA CTGAGGATATTTAAAATTCATTT  
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGA ACTAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTCACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCCACCTCCGGA ACTTCTGACCTCTGTTTCCTCCGTCCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCCTCGTCTCACCCCTTTACACTCACATTTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA



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## **FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVWEGWLMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGP SHYMARYSTSAPAI SRGPSEYPTKNYV
```

### **Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATT TTTATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGGACTCTTGCCACAACCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
TGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGCCAAAGCATAACCTTCTGGGAACTTCAGGAGTCTCTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGCGCTGGGCA  
AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

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## **FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER

AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL

FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

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## **FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGGCTGCCTCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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## **FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYD  
EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTGAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTCACAGCAACACCGCCAG  
CCCCGGACTCCCCGCAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG  
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCCTGCCCCGCCGGGGTCCGAGCCCCGGCCCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCCGA  
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA  
AAAAAAA



## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPCCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

[illegible]

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## **FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHC AKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
TTGGGGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGCACACGC  
TGTTGGCAAATGTCAGGACCAGGTTAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCA  
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
CAGACTCCAGTTTCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGT  
TGCACCCTCCCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT  
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTACGCTGGACCCAC  
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCCAGGTGCGG  
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
CCAGGGCCTTTCCTGAAGGAGATCATCCTCGTGAGCAGCCTCAGCCAGCAAGGACAACCTCAAG  
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGGTGCCATCAGGGCCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
TCATGGATGCCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT  
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGGAAC  
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTCAAGGCCTGGCTCTGTGGTG  
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT  
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGG  
GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTGCGACATTCCACTGG  
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
AGGAAGGAGATTCACTTTGGCAGCCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  
GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAATTTTGGCCATC  
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTATGAAGCTGATCCTTTTGTGT  
GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
TCACACCTTATTTTATTGACTGCTGGCTGCTTA

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## **FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRWDGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPPRAFLKEIILVDDLSSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP  
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGENLELSFKAWLCGGSVEILPCSRVGHYQNDQSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLLGCRTFWFLANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCAVRQEQVILQNCTEEGLAIHQHWDFFQENGMIVHILSGKCMEEAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGAC**ATGGA**  
GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCACACAGCCCCAGCC  
CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTTCATGTGTGCGTGTGGGAGCGAGC  
ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTTCGGCAAGTCCTGCCTGGCACTG  
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGGCCCTCATCCCAATACCCCTGGGCT  
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
ATTTCTGGACTATGGTTTTGACGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATT  
CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCACTCTATGTACAAATTACCATCTCCAT  
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCC  
TGACCATGAGGAGCCCCGAGGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
CCTTCAGTTGAACCGG**TG**AGGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC  
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC  
CTTCTCCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCC  
TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC  
CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT  
TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCAATGTTGGGGTGCAGCC  
AAGCAGGAGGCCAAGGGGCGGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTTGACACACCACCGGAACACTCCCCAGCC  
CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
GGTCCCTGTCCCCACCCTTGTGCACTCACATGAAAGCCTTGCACTCACCTCCACCTTCAC  
AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATAACCGCTCCGCTCAGCTGACTCT  
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG  
TGGTCAGCGTTTCCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG  
TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC  
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGGCCCTCATCGGTCTATGG  
TCTCGTCCCATTCACACCATTTGTTTCTCTGTCTCCCATCCTACTCCAAGGATGCCGGCA  
TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA  
CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA  
AGGGACTCCCATTGCCCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG  
TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT  
CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGACTCCCTCCTGTCCCCCTCCTTT  
CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTTGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT  
CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTCCTTCCCTTCCCTTCCCTGGCTCCTAGGCT  
GTGATATATATTTTTGTATTATCTTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
GGATGTAAGTTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

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## **FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV  
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## FIGURE 205

GTTAACACGCGCAGTCTCTCGTGCCTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACC GTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTCTGGCGCTCGTGGTCTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAAAAA



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## **FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG  
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 91-110

#### **Glycosaminoglycan attachment site.**

amino acids 44-47

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

#### **N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCGACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGACCTCCCCTAAGTAGCCC  
CCAGAGGCGCTGGGAGTGTGGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG  
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGCTCCCCGCTTCCAC  
CTGGCTGTGTCGCGGTAGGGCGGGGCCGTGGGTTAGGGGCGCACCACCTTCCAAGCCTGTGT  
CCCACAGGTCTCGGCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC  
TGGCACAAGTAAGTCCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACAACCTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

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## **FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCT  
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC  
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
TAGCATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACCTG  
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCG  
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAATAAGGAGTCTCAACTGCCAG  
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATTTGTTGAAAGAAAATCG  
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACATCATATGGCC  
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG  
GATCACTAGGCCTGCCAACCACACACACACGACGTGCACACACGCACGCACGCGTGCACAC  
ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAAATCTCGTTTTCTC  
TTCTTCCTTCTTTTAAATTTTATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT  
TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT  
TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
CCTGAACCTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC  
TATGTAAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

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## **FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSTFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQKGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTGCTGGCGGCGGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGAGAGCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTTCAAGAACATTCCTTTTACCATCATTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAACTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACT  
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCATATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

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## **FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGA CTGCCCGGGCTGCCGCC  
CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
TCTCGGCCACGGCTGGGTCGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCGACCCTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTTCTGTACACAAGATTACTGATTTCCCATTTAAGTGGAATTGCG  
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA  
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT  
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGGTTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
TTAACACTATTTTATTAATTAAGTCAAATTTCTTTGTTTCCATTCCAAAATCAACCTGC  
CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA  
TGTTTATAAAGTAAAAAAA



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## **FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQEQSLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
GGTGC GCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGCACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCGGTGGTGACGCACCCCGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCGAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGG  
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATAACATTGAAATGTG  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG  
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

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## **FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA  
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVS VVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQE QKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCTCCGGGGGGCCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA  
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA  
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGA  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCCGACCGCCGC  
GTGCTGCTGCTGGGCACCATAAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTGAGCATTGCTCTG  
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT  
GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAA

**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
EQAGVLNWFRVPLHSLACLGLLVLHDSRKTGTRNMFSCSAVMVMALLAVVGLEFTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATG  
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTTCTTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGGTAGAAAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT  
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
AGTGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTACTGACTTTTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

[illegible]



**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538  
><subunit 1 of 1, 116 aa, 1 stop  
><MW: 12910, pI: 6.41, NX(S/T): 1  
MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW  
CCQTHDCCYDHLKTQGCGLYKDNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCCAGGGGGCCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAAC TCACCCGTGGGTTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

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## **FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK  
LGDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
GAACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT  
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
TATTTGTTCTTGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
CCCAAGGGGTCCAATTTTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG  
ACAGGGGCTGTGATGCAACTGGCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA  
CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
ATAGCCCCACTGCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT  
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAAGCTGGATGTGCC  
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT  
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
TGGAAGCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT  
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAATCAGTGTCTATAG  
GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
GAAGCTTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA  
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTG  
AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCCAAAGAGCTGCAAGG  
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCAT  
GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG  
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT  
GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAAACCCACCAACACGAGACCAGCGAGA  
TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC  
TGGTGACTATCAAGGGAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTG  
CAAGATCCTTCCTTGTCCGTTTTAGTGCATTCATAATACTGGTCATTTTCTCTCATACATA  
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGCTCCGGTTTAAATATAA  
TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTCGCATTTGTTTTAAGATAAACT  
TCTTTCATAGGTAAAAA

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## **FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVELLTMSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL  
DLGYNRIRSLARNVVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTM  
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKEQGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLN  
GTGPCTYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
TAAATATGTCAAGATCCAGACTTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCCCTGCTCCATGTTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCTTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGTATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

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## **FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAAGTCAGATGCCCTTTTAACT  
 CCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA  
 CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGCTTGTATTTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGTAAGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGGAAC  
 TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTCTTTTCAAGCAAGTCTGTTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACCTGAGTGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCT  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCAATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTGTACTATATTTTGTATTTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAGTTTAAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATATGGTCT  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAATAAGAACATTTAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT  
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCAATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT



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## **FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL  
VPVTTNKRTNVSGSIR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
 CATGCCGTGGCCCCCTGCTGCTGCTGCTGCGCGTGAGTGGGGCCAGACAACCCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGCTGCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTGCTG  
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG  
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
 CACAACCTCATTACCCGCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
 TGCCTACCTGAGCCTGGATGGGAACCTCTAGCTGTTCATTGGTCCGGGTGCCTTCGCGGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAAC  
 GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCCCTGCACTGCGTAGACACCCGGAATCTGCTGCCAGGGGCCCCACC  
 ATCTTGTGACAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCCTGGGCTGCCTCAG  
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCACTGGGGAGCCCGCAGGCCTATGTGGCA  
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT  
 GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCCACTCAGGGGCGAGTT  
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA  
 ATAAGCCCCACCCTCCCCGCTGGGCTCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC  
 CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGCCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC  
 CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCTGGGCTGTTTCCTTAGTCTTCATTTTA  
 TAAAAGTTGTTGCCTTTTAAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT  
 ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
 CCATCATCTATCTAACCGGTCTTGATTTAATAAACACTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSFAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSLQELDLSGTNLVPLPEALLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC  
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT  
ATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTTTATACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGGCT  
AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
CCAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTWCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTTCAGATGCAAAT  
GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTG  
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTTAA

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## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH  
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA  
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGGTTTTAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA



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## **FIGURE 238**

' MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
CTGGCGGCCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
GGTCAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
**GATG**GAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
TGTTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
GCCTCGCCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGGTGCACTGGTGCTGGTGG  
CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG  
GGGAGTTCCTACGCAAAACAACTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG  
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTT**TAGGGT**GGC  
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGC  
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCCTACCCGGAAGACC  
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG  
ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

#### **N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC  
CTGCACCCCTTCCTGGGACACTATGTGTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA  
GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG  
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
CCTTCTCCTGGCTGTTTATTTTATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA  
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA  
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG  
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG  
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTTGATCAATA  
TATTTGGAAATTAAAGTTTCTGACTTT

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## **FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812  
><subunit 1 of 1, 337 aa, 1 stop  
><MW: 37668, pI: 6.27, NX(S/T): 1  
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPAYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ  
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQCTL  
FSTEEEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 291-310

#### **N-glycosylation site.**

amino acids 213-216

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

[illegible]

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## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFVVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG  
GCAGCCGGGAGCCATGCGACCCAGGGCCCCGCCCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
GGATCCCAGGTCCGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG  
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAATA  
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
GGTTTCAATATTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAATA  
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAAT  
AAAAATTATTTCCAACA



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## **FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217